



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 112948**

**TO: Celine Qian**  
**Location: rem/2a89**  
**Art Unit: 1636**  
**Thursday, January 29, 2004**

**Case Serial Number: 09/780532**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**CM1-6B02**  
**Phone: 305-9203**

**[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)**

### **Search Notes**

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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Access DB# 112948

C RFE

# RECEIVED SEARCH REQUEST FORM

Scientific and Technical Information Center  
JUN 28 2001

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 1/28/04  
An Unit: 1636 Phone Number: 2-0777 Serial Number: 09/780532  
Mail Box and Bldg Room Location: Rensselaer Results Format Preferred (circle): PAPER ~~DISK~~ ~~E-MAIL~~  
2A39

If more than one search is submitted, please prioritize searches in order of need: 1/1 E

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Trade molecules and uses related thereto

Inventors (please provide full names): Clive Wood et al.

Earliest Priority Filing Date: 2/11/00

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for SEQ ID NO: 2 (both commercial and interference database)  
1  
417ATA

RECEIVED  
JUN 29 2001  
(6113)

## STAFF USE ONLY

Searcher: 1129/04 NA Sequence (#): \_\_\_\_\_ STN: \_\_\_\_\_  
Searcher Phone: 11/30/01 AA Sequence (#): 1 Dialog: AB5505P

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .nupm and .nupn.

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

*Because they contain data that is confidential, the results of Pending database searches should not be left in the case.*

**BEST AVAILABLE COPY**

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2004, 21:32:31 ; Search time 46 Seconds  
(without alignments)  
1438.891 Million cell updates/sec

Title: US-09-780-532A-2

Perfect score: 2256

Sequence: 1 MALKVLEQKEFTFLVLL.....LDQSGAIHPATQTSIQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.\*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
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3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	417	22 AAU04492	Human TRADE-alpha
2	2255	100.0	417	20 AAU98146	Human TRAIN-R. Ho
3	2255	100.0	417	21 AAB33474	Human PRO4333 prot
4	2255	100.0	417	22 AAU29260	Human PRO polypept
5	2255	100.0	417	22 AAB82412	Human tumour necro
6	2255	100.0	417	23 ABB95567	Human angiogenesis
7	2255	100.0	417	23 ABB84961	Human PRO4333 prot
8	2255	100.0	417	23 AAU83701	Human PRO protein,
9	2255	100.0	417	24 ABU71348	Human PRO4333 prot

10	2255	100.0	417	24 ABU65805	Human secreted/tra
11	2255	100.0	417	24 ABU66138	Novel human secret
12	2255	100.0	417	24 ABU67642	Human secreted/tra
13	2255	100.0	417	24 ABU65500	Human PRO polypept
14	2255	100.0	417	24 ABU58636	Human PRO polypept
15	2255	100.0	417	24 ABU56172	Human secreted/tra
16	2255	100.0	417	24 ABU57167	Human PRO polypept
17	2255	100.0	417	24 ABU10746	Human secreted/tra
18	2233	99.0	423	20 AAU85724	Novel protein (Clo
19	2233	99.0	423	22 AAU04493	Human TRADE-beta p
20	2231	98.9	417	19 AAU70386	Amino acid sequenc
21	2230	98.8	423	20 AAU93581	Human hAPO4-alpha
22	2230	98.8	423	21 AAB23547	Human Troy protein
23	2222	98.5	423	19 AAU70387	Amino acid sequenc
24	1567.5	69.5	416	21 AAB23546	Murine Troy protei
25	1567.5	69.5	416	22 AAU04494	Murine TRADE polyp
26	1565.5	69.4	416	20 AAU93579	Mouse mAPO4-alpha
27	1553.5	68.9	328	20 AAU06400	Human NTR-5 recept
28	973	43.1	214	20 AAU06522	Mouse STRIFE1 (tan
29	973	43.1	214	20 AAU98145	Mouse TRAIN-R (lon
30	973	43.1	214	20 AAU93580	Mouse mAPO4-alpha
31	973	43.1	214	21 AAB23548	Murine dTroy prote
32	973	43.1	214	23 AAB78030	Human STRIFE1. Ho
33	865	38.3	210	20 AAU22223	Human TNFR superfa
34	865	38.3	210	21 AAB28555	Human TNFR soluble
35	857	38.0	150	20 AAU98148	TRAIN-R short, sol
36	783	34.7	160	20 AAU06399	Mouse NTR-5 recept
37	752	33.3	166	22 AAU24239	Human EST encoded
38	721	32.0	150	20 AAU06523	Mouse STRIFE2 (tan
39	721	32.0	150	20 AAU22224	Mouse TNFR superfa
40	721	32.0	150	20 AAU98144	Mouse TRAIN-R (sho
41	721	32.0	150	20 AAU93583	Mouse mAPO4-gamma
42	721	32.0	150	21 AAB28556	Mouse TNFR soluble
43	721	32.0	150	21 AAU77465	Murine Rank-like p
44	721	32.0	150	23 AAB78031	Human STRIFE2. Ho
45	721	32.0	150	24 AAU26528	Mouse RANK-like pr

#### ALIGNMENTS

RESULT 1  
AAU04492  
ID AAU04492 standard; Protein; 417 AA.

AC AAU04492;

XX 24-OCT-2001 (first entry)

DT Human TRADE-alpha polypeptide.

DE TRADE-alpha; TRADE-beta; proliferation; apoptosis; inflammation; liver;  
KW NFkB signalling pathway; JNK signalling pathway; neoplasia; carcinoma;  
KW necrosis; adenocarcinoma; lung; brain; intestine; Crohn's disease;  
KW prostate; myeloid leukemia; autoimmune lymphoproliferative syndrome; human;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; epithelial cell.

OS Homo sapiens.

XX	Key	Location/Qualifiers
XX	Key	1..25
XX	Key	/note= "Signal peptide"
XX	Key	1..168
XX	Key	/note= "Extracellular domain"
XX	Key	26..417
XX	Key	/note= "Mature TRADE-alpha protein"
XX	Key	29..63
XX	Key	/note= "Cysteine-rich domain #1"
XX	Key	72..114
XX	Key	/note= "Cysteine-rich domain #2"
XX	Key	105..108
XX	Key	/note= "Asn is N-glycosylated"
XX	Key	114..139

```

FT FT Domain /note= "Cysteine-rich domain #3"
FT FT 137..168
FT FT /note= "Serine/threonine/proline-rich domain"
FT FT 169..192
FT FT /note= "Transmembrane domain"
FT FT 193..417
FT FT /note= "Intracellular domain"
FT FT Modified-site 200..203
FT FT /note= "Ser is phosphorylated by CAMP/CGMP-dependent
FT FT protein kinase"
FT FT Modified-site 205..207
FT FT /note= "Ser is phosphorylated by protein kinase C"
FT FT Modified-site 207..213
FT FT /note= "Tyrosine is phosphorylated by tyrosine kinase"
FT FT Modified-site 215..220
FT FT /note= "Gly is N-myristoylated"
FT FT Domain 218..417
FT FT /note= "TRADE-related death effector domain"
FT FT Modified-site 219..222
FT FT /note= "Ser is phosphorylated by casein kinase II"
FT FT Modified-site 238..241
FT FT /note= "Ser is phosphorylated by CAMP/CGMP-dependent
FT FT protein kinase"
FT FT Modified-site 325..328
FT FT /note= "Ser is phosphorylated by casein kinase II"
FT FT WO200158954-A2.
FT FT 16-AUG-2001.
FT FT 09-FEB-2001; 2001WO-US04238.
FT FT 11-FEB-2000; 2000US-0181922.
FT FT 14-FEB-2000; 2000US-0182148.
FT FT (GEMY ) GENETICS INST INC.
FT FT Wood C, Chaudhary D, Long A;
FT FT WPI; 2001-502708/55.
FT FT N-PSDB; AAS08983.
FT FT Modulation of cell proliferation for the treatment of cancer comprises
FT FT contacting a cell with a TRADE family peptide which modulates cell
FT FT peptide activity or expression
FT FT Disclosure; Fig 1; 173pp; English.
FT FT
FT FT The sequence represents a human TRADE-alpha polypeptide. TRADE molecules
FT FT are useful for the regulation of cellular processes such as cell
FT FT proliferation (e.g., by inducing either proliferation or apoptosis), via
FT FT the NFkB and JNK signalling pathways. A cell can be contacted with an
FT FT agent that modulates the expression of a TRADE-alpha or TRADE-beta
FT FT polypeptide, hence altering the rate of proliferation. Modulating agents
FT FT may also be used in the detection of TRADE associated proliferative
FT FT disorders such as inflammation, neoplasia, apoptosis or necrosis. The
FT FT treatable neoplasia is a carcinoma or an adenocarcinoma present in
FT FT epithelial cells e.g., of the lung, liver, brain, intestine or prostate.
FT FT Other TRADE associated disorders include Crohn's disease, myelokathexis,
FT FT autoimmune lymphoproliferative syndrome, Alzheimer's disease and
FT FT amyotrophic lateral sclerosis.
FT FT
FT FT Sequence 417 AA;

Query Match 100.0%; Score 2256; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.9e-192;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLEQKTFPTLLVLLGLYSCKVTCSEGDCRQOEFRDRSGNCVPCNOCGPMELSK 60
Db 1 MALKVLEQKTFPTLLVLLGLYSCKVTCSEGDCRQOEFRDRSGNCVPCNOCGPMELSK 60
Qy 61 ECGFGYGEDAQCVTRLHRFKEDWGQKCPCLDCAVNNRFQKANCATSDAICGDCPLG 120

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CC necrosis factor receptor family member termed TRAIN-R that is  
 CC expressed at low levels in every tissue and cell line tested thus  
 CC far, with higher expression detected in heart, prostate, ovary,  
 CC testis, peripheral blood lymphocytes, thyroid and adrenal gland.  
 CC Cell death can be induced by administering an agent capable of  
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method  
 CC of treating, or reducing, the advancement, severity or effects of  
 CC an immunological disease in a mammal comprises administering a  
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,  
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to  
 CC produce a fusion protein which may be targeted to various sites.  
 CC It can be used in binding assays, and to identify antagonists and  
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the  
 CC severity of an immune response or to treat cancer. TRAIN-R  
 CC blocking agents can also be used to reduce the severity or effects  
 CC of an immunological disease (all claimed).  
 XX SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 20; Length 417;  
 Best Local Similarity 99.8%; Pred. No. 2.4e-192;  
 Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLLSEQKTFPFLVLLVGLSKVTCESGDCRQEFDRSGNVCVPCNCGPGMELSK 60  
 Db 1 MALKVLLSEQKTFPFLVLLVGLSKVTCESGDCRQEFDRSGNVCVPCNCGPGMELSK 60  
 Qy 61 ECGFGYGDAQCVCRLHRFKEDWGFQCKPCDCAVNRFKQNCATSATSDAICGDCUPG 120  
 Db 61 ECGFGYGDAQCVCRLHRFKEDWGFQCKPCDCAVNRFKQNCATSATSDAICGDCUPG 120  
 Qy 121 FYRKTGLVGFQDMCVCPGDPFPPEPHPCASKVNLVKIATSSPRDTALAIVCSALAT 180  
 Db 121 FYRKTGLVGFQDMCVCPGDPFPPEPHPCASKVNLVKIATSSPRDTALAIVCSALAT 180  
 Qy 181 VLLALLILCVLYCKRQFKPSLSRQDIQYNGSELSCFDRPOLHYAHRAACQCRRD 240  
 Db 181 VLLALLILCVLYCKRQFKPSLSRQDIQYNGSELSCFDRPOLHYAHRAACQCRRD 240  
 Qy 241 SVQTCGVRLLPSMCCBEACSPNATLGGVHSAASLQARNAGPAGEMVPTFFGSLTOSI 300  
 Db 241 SVQTCGVRLLPSMCCBEACSPNATLGGVHSAASLQARNAGPAGEMVPTFFGSLTOSI 300  
 Qy 301 CGEFSDAWPLMNPNGDNI SFCDSPYELTGEDIHSLNPELESSTLSLNSSSQDLVGAV 360  
 Db 301 CGEFSDAWPLMNPNGDNI SFCDSPYELTGEDIHSLNPELESSTLSLNSSSQDLVGAV 360  
 Qy 361 PVQSHSENFTATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATOTSLOEA 417  
 Db 361 PVQSHSENFTATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATOTSLOEA 417

RESULT 3  
 AAB33474  
 ID AAB33474 standard; Protein; 417 AA.  
 XX AC AAB33474;  
 XX DT 29-JAN-2001 (first entry)  
 XX DE Human PRO4333 protein UNQ1888 SEQ ID NO:286.  
 XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antinaemic; hepatotropic; virucide; antiporiatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;

KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.  
 XX WO200053758-A2.  
 XX 14-SEP-2000.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 10-MAR-1999; 99US-0123618.  
 XX 12-MAR-1999; 99US-0123957.  
 XX 13-MAR-1999; 99US-0125775.  
 XX 12-APR-1999; 99US-0128849.  
 XX 20-APR-1999; 99WO-US08615.  
 XX 28-APR-1999; 99US-0131445.  
 XX 04-MAY-1999; 99US-0132371.  
 XX 14-MAY-1999; 99US-0134287.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 08-SEP-1999; 99WO-US20594.  
 XX 13-SEP-1999; 99WO-US20944.  
 XX 15-SEP-1999; 99WO-US21090.  
 XX 15-SEP-1999; 99WO-US21547.  
 XX 05-OCT-1999; 99WO-US23089.  
 XX 29-OCT-1999; 99US-0162506.  
 XX 29-NOV-1999; 99WO-US28214.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 30-NOV-1999; 99WO-US28409.  
 XX 01-DEC-1999; 99WO-US28301.  
 XX 01-DEC-1999; 99WO-US28634.  
 XX 02-DEC-1999; 99WO-US28551.  
 XX 02-DEC-1999; 99WO-US28564.  
 XX 02-DEC-1999; 99WO-US28585.  
 XX 16-DEC-1999; 99WO-US30095.  
 XX 20-DEC-1999; 99WO-US30999.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 06-JAN-2000; 2000WO-US00277.  
 XX 06-JAN-2000; 2000WO-US00376.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 22-FEB-2000; 2000WO-US04414.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI; 2000-572271/53.  
 XX N-PSDB; AAC58639.  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX Claim 33; Fig 122; 309pp; English.  
 XX The present invention describes sixty four human PRO proteins which can  
 XX be used in the treatment of immune related diseases. The human PRO  
 XX proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 XX treating and diagnosing immune related disorders. The disorders are  
 XX selected from systemic lupus erythematosus, rheumatoid arthritis,  
 XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

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CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 21; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKVLEQETFTLLVLLGYLSCKVTCBSGDCRQEFDRSGNCVPCNQCQGMELSK 60
DB 1 MALKVLEQETFTLLVLLGYLSCKVTCBSGDCRQEFDRSGNCVPCNQCQGMELSK 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDLPG 120
DB 61 ECGFGYGEDAQCVTCRLHRFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDLPG 120

QY 121 FYRKTUUVGQDMCEVPCGPPPPYEPHCASKNVLVKIATASSPRDTALAAVICSALAT 180
DB 121 FYRKTUUVGQDMCEVPCGPPPPYEPHCASKNVLVKIATASSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVYCKRQFWEKPSLSLSODIYNGSELSFCFDRPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKRQFWEKPSLSLSODIYNGSELSFCFDRPOLHEYAHRACCCRRD 240

QY 241 SVQTCGVRLLPSCCCEACSPNATILGCGVHSAASIQARNAGPAGEMVPTFFGSLTQSI 300
DB 241 SVQTCGVRLLPSCCCEACSPNATILGCGVHSAASIQARNAGPAGEMVPTFFGSLTQSI 300

QY 301 CGEFSDAWPLMNPWGDNISFCDSYPDLTGEDIHSLNPELSSTLDSNSSQDLVGGAV 360
DB 301 CGEFSDAWPLMNPWGDNISFCDSYPDLTGEDIHSLNPELSSTLDSNSSQDLVGGAV 360

QY 361 PVQSHSENFTAATDLSRYNNLTVESASTODALTMRSQLDQESGAIHPATQTSIQEA 417
DB 361 PVQSHSENFTAATDLSRYNNLTVESASTODALTMRSQLDQESGAIHPATQTSIQEA 417

RESULT 4
AAU29260
ID AAU29260 standard; Protein; 417 AA.
XX
XX AAU29260;
XX AC
XX 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #237.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06520.
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
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PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX N-PSDB; AAS46161.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -
XX
XX Claim 11; Fig 474; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
XX detect the presence of a tumour in a mammal by comparing the level of
XX expression of a PRO polypeptide in a test sample of cells from the animal
XX and a control sample of normal cells, whereby a higher level of
XX expression in the test sample indicates the presence of a tumour in the
XX mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
XX and rabbits but are preferably human. The polypeptides can be used to
XX stimulate tumour necrosis factor (TNF) alpha release from human blood,
XX when contacted with it. A specific polypeptide can be used to stimulate
XX the proliferation or differentiation of chondrocyte cells. The PRO
XX proteins can be used to determine the presence of tumours and also
XX susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders.
XX
XX Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 22; Length 417;
```

Best Local Similarity 99.8%; Pred. No. 2.4e-192; Mismatches 0; Indels 0; Gaps 0; Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKVLLLEQEKTFFTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNOCGPGMELSK 60  
DB 1 MALKVLLLEQEKTFFTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNOCGPGMELSK 60

QY 61 ECGFGYGEDAQCVTCLRLHFKEDWGFKCKPCLDCAVNNRFQKANCATSATSDAICGDCPLG 120  
DB 61 ECGFGYGEDAQCVTCLRLHFKEDWGFKCKPCLDCAVNNRFQKANCATSATSDAICGDCPLG 120

QY 121 FYRKTCLVGFQDMCEVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180  
DB 121 FYRKTCLVGFQDMCEVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVIYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240  
DB 181 VLLALLILCVIYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

QY 241 SVQTCGVPVRLLPSCMCCEACSPNPATLGGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300  
DB 241 SVQTCGVPVRLLPSCMCCEACSPNPATLGGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

QY 301 CGEFSDAWPLMQNPMWGDNISFCDSYPBELTGEDIHSLNPELESSTLSDSNSQDLVGAV 360  
DB 301 CGEFSDAWPLMQNPMWGDNISFCDSYPBELTGEDIHSLNPELESSTLSDSNSQDLVGAV 360

QY 361 PVQSHSENFATDLRYNNLTVESASTQDALTMRSQDQESGATIHHPATQTSLQEA 417  
DB 361 PVQSHSENFATDLRYNNLTVESASTQDALTMRSQDQESGATIHHPATQTSLQEA 417

RESULT 5  
AAB82412  
ID AAB82412 standard; Protein; 417 AA.  
XX AAB82412;  
XX  
DT 06-AUG-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor R248.  
XX  
KW Tumour necrosis factor receptor; R248; human; antiarthritic;  
KW antirheumatic; antiasthmatic; antidiabetic; antiinflammatory.  
KW asthma; rheumatoid arthritis; diabetes; inflammation; infection;  
KW chronic obstructive pulmonary disease; nephritis; heart disease;  
KW therapy.

XX OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein 26..417  
FT Region 1..168  
FT Region 169..192  
FT Region 193..417  
FT Domain 31..72  
FT Domain 75..114  
FT Domain 117..149  
FT Domain 105  
FT Modified-site /note= "N-glycosylated"  
FT Binding-site 34..146

FT /note= "predicted ligand binding site"  
XX WO200138526-A1.  
XX 31-MAY-2001.  
XX 21-NOV-2000; 2000WO-GB04438.  
XX 23-NOV-1999; 99GB-0027681.  
XX (GLAX ) GLAXO GROUP LTD.  
XX Kitson JDA;  
PI WPI; 2001-367687/38.  
DR N-PSDB; AAF90463.  
DR Novel isolated human tumour necrosis factor receptor polypeptide, R248,  
PT or its variant capable of activating NF-kappaB useful for treating  
PT asthma, rheumatoid arthritis, heart disease, nephritis, diabetes -  
XX Claim 1(i); Fig 1; 34pp; English.  
XX  
CC The present sequence is that of novel human tumour necrosis factor  
CC receptor R248. R248 is expressed in activated lymphocytes but not  
CC in resting lymphocytes, suggesting a role in chronic inflammatory  
CC diseases, such as rheumatoid arthritis and asthma. Expression in  
CC chondrocytes indicates a role in bone metabolism, which is important  
CC in the bone destruction observed in rheumatoid arthritis,  
CC osteoarthritis and steroid mediated bone erosion. Expression of the  
CC receptor in epithelial cell layers in liver gut and pancreas  
CC implicates R248 in inflammation associated with these tissues.  
CC R248 is capable of activating NF-kappaB. cDNA (see AAF90463)  
CC encoding R248 was obtained by PCR amplification of human aortic  
CC smooth muscle cell cDNA using R248-specific primers. R248 is a  
CC screening target for the identification of novel pharmaceutical  
CC agents which modulate the activity of the receptor, or which  
CC used in a claimed method of treating a subject having an immune or  
CC inflammatory disorder or smooth muscle cell disorder, such as  
CC asthma, rheumatoid arthritis, chronic obstructive pulmonary disease,  
CC diabetes, inflammation associated with bacterial or viral infection,  
CC nephritis and heart disease.  
XX SQ Sequence 417 AA;  
Query Match 100.0%; Score 2255; DB 22; Length 417;  
Best Local Similarity 99.8%; Pred. No. 2.4e-192;  
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKVLLLEQEKTFFTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNOCGPGMELSK 60  
DB 1 MALKVLLLEQEKTFFTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNOCGPGMELSK 60

QY 61 ECGFGYGEDAQCVTCLRLHFKEDWGFKCKPCLDCAVNNRFQKANCATSATSDAICGDCPLG 120  
DB 61 ECGFGYGEDAQCVTCLRLHFKEDWGFKCKPCLDCAVNNRFQKANCATSATSDAICGDCPLG 120

QY 121 FYRKTCLVGFQDMCEVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180  
DB 121 FYRKTCLVGFQDMCEVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVIYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240  
DB 181 VLLALLILCVIYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

QY 241 SVQTCGVPVRLLPSCMCCEACSPNPATLGGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300  
DB 241 SVQTCGVPVRLLPSCMCCEACSPNPATLGGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

QY 301 CGEFSDAWPLMQNPMWGDNISFCDSYPBELTGEDIHSLNPELESSTLSDSNSQDLVGAV 360  
DB 301 CGEFSDAWPLMQNPMWGDNISFCDSYPBELTGEDIHSLNPELESSTLSDSNSQDLVGAV 360

OY 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOEA 417  
 DB 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQLDOESGAVIHPATQTSLOEA 417

## RESULT 6

ABB95567  
 ID ABB95567 standard; Protein; 417 AA.

XX ABB95567;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO4333 SEQ ID NO: 290.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytosstatic; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0684610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 30-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 30-MAY-2001; 2001WO-US17443.

XX 01-JUN-2001; 2001WO-US17800.

XX 28-JUN-2001; 2001WO-US19692.

XX 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

DR N-PSDB; ABL95705.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 290; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 23; Length 417;  
 Best Local Similarity 99.8%; Pred. No. 2.4e-192;  
 Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCEGDCRQOEFDRSGNCVPCNQCQPGMELSK 60

DB 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCEGDCRQOEFDRSGNCVPCNQCQPGMELSK 60

OY 61 ECGFGYGEDAQCVTCRLHRFKEDWGFKCKPCLDCAVNRFOKANCATSDAICGDCPLG 120

DB 61 ECGFGYGEDAQCVTCRLHRFKEDWGFKCKPCLDCAVNRFOKANCATSDAICGDCPLG 120

OY 121 FYRKTCLVGFQDMECVPCGDPPTPPYPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180

DB 121 FYRKTCLVGFQDMECVPCGDPPTPPYPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180

OY 181 VLLALLILCVYCKRQFMKKPSWSIRSQDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

DB 181 VLLALLILCVYCKRQFMKKPSWSIRSQDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

OY 241 SVOTCGPVRLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMWPTFFGSLTQSI 300

DB 241 SVOTCGPVRLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMWPTFFGSLTQSI 300

OY 301 CGEFSDAWPLMQNPMGGDNISFCDSPYELTGEDIHSLNPELESSTLDNSSDQLVGGAV 360

DB 301 CGEFSDAWPLMQNPMGGDNISFCDSPYELTGEDIHSLNPELESSTLDNSSDQLVGGAV 360

OY 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOEA 417

DB 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQLDOESGAVIHPATQTSLOEA 417

RESULT 7

ABB84961

ID ABB84961 standard; Protein; 417 AA.

XX

AC ABB84961;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO4333 protein sequence SEQ ID NO:290.

XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US19692.

XX PR 23-JUN-2000; 2000US-213637P.

XX PR 20-JUL-2000; 2000US-219556P.

XX PR 25-JUL-2000; 2000US-220624P.

XX PR 25-JUL-2000; 2000US-220664P.

XX PR 28-JUL-2000; 2000WO-US20710.

XX PR 02-AUG-2000; 2000US-222695P.

XX PR 17-AUG-2000; 2000US-064357.

XX PR 23-AUG-2000; 2000WO-US23522.

XX PR 24-AUG-2000; 2000WO-US23328.

XX PR 07-SEP-2000; 2000US-230978P.

XX PR 18-SEP-2000; 2000US-0664610.

XX PR 18-SEP-2000; 2000US-0665350.

XX PR 24-OCT-2000; 2000US-242922P.

XX PR 08-NOV-2000; 2000US-0709238.

XX PR 08-NOV-2000; 2000WO-US30952.

XX PR 10-NOV-2000; 2000WO-US30873.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 20-DEC-2000; 2000US-0747259.

XX PR 20-DEC-2000; 2000WO-US34956.

XX PR 22-JAN-2001; 2001US-0767609.

XX PR 28-FEB-2001; 2001US-0796498.

XX PR 28-FEB-2001; 2001WO-US06520.

XX PR 01-MAR-2001; 2001WO-US06656.

XX PR 09-MAR-2001; 2001US-0802706.

XX PR 14-MAR-2001; 2001US-0808689.

XX PR 22-MAR-2001; 2001US-0816744.

XX PR 05-APR-2001; 2001US-0828366.

XX PR 10-MAY-2001; 2001US-0854208.

XX PR 10-MAY-2001; 2001US-0854280.

XX PR 25-MAY-2001; 2001US-0866028.

XX PR 25-MAY-2001; 2001US-0866034.

XX PR 30-MAY-2001; 2001WO-US17092.

XX PR 30-MAY-2001; 2001US-0870574.

XX PR 30-MAY-2001; 2001WO-US17443.

XX PR 01-JUN-2001; 2001WO-US17800.

XX FA (GETH ) GENENTECH INC.

XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WIPI; 2002-090516/12.

XX DR N-ESDB; ABL88216.

XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 290; 565pp; English.

XX PS

XX XX

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cariant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related restenosis, degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 2255; DB 23; Length 417;

Best Local Similarity 99.8%; Pred. No. 2.4e-192;

Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLLLEQEKTFLLVLLGLYLSCKVTCSGCRQOEPRDRSGNCVPCNCGPMELSK 60

Db 1 MALKVLLLEQEKTFLLVLLGLYLSCKVTCSGCRQOEPRDRSGNCVPCNCGPMELSK 60

Qy 61 ECGFGYGEDAQCVTCRLHREFKEDWGFOCKPKCLDCAVNNRFQKANCATSDAICGDCPLG 120

Db 61 ECGFGYGEDAQCVTCRLHREFKEDWGFOCKPKCLDCAVNNRFQKANCATSDAICGDCPLG 120

Qy 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASPRDTALAAVTCALAT 180

Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASPRDTALAAVTCALAT 180

Qy 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAHCCQCRD 240

Db 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAHCCQCRD 240

Qy 241 SVQTCGVRLLPSMCCCEACSPNPATILGCGVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300

Db 241 SVQTCGVRLLPSMCCCEACSPNPATILGCGVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300

Qy 301 CGEFSDAWPLMNPMPMGDNI SFCDSPYELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360

Db 301 CGEFSDAWPLMNPMPMGDNI SFCDSPYELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360

Qy 361 PVQSHSENFTAATDLGRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

Db 361 PVQSHSENFTAATDLGRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

RESULT 8

AAU83701

ID AAU83701 standard; Protein; 417 AA.

XX AAU83701;

XX 08-MAY-2002 (first entry)

XX Human PRO protein, Seq ID No 220.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.

XX Homo sapiens.

XX OS

XX WO200208288-A2.

XX 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US21066.

XX XX

PR	20-JUL-2000; 2000US-219556P.	Db	181	VLLALLILCVYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD	240
PR	25-JUL-2000; 2000US-220585P.	Qy	241	SVQTCGPVRLPSMCCCEACSPNPATILGCGVHSAASLOARNAGPAGEMVPTFFGSLTQSI	300
PR	25-JUL-2000; 2000US-220605P.	Db	241	SVQTCGPVRLPSMCCCEACSPNPATILGCGVHSAASLOARNAGPAGEMVPTFFGSLTQSI	300
PR	25-JUL-2000; 2000US-220607P.	Qy	301	CGEFSDAWPLMQNPMGDNISFCDSYPGLTGTEDIHSLNPELESSTLSDNSSODLVGGAV	360
PR	25-JUL-2000; 2000US-220624P.	Db	301	CGEFSDAWPLMQNPMGDNISFCDSYPGLTGTEDIHSLNPELESSTLSDNSSODLVGGAV	360
PR	25-JUL-2000; 2000US-220638P.	Qy	361	PVQSHSENFTAATDLGRYNNNTLVESASTQDALTMRSQDQESGAIHPATQTSIQA	417
PR	25-JUL-2000; 2000US-220664P.	Db	361	PVQSHSENFTAATDLGRYNNNTLVESASTQDALTMRSQDQESGAIHPATQTSIQA	417
PR	25-JUL-2000; 2000US-220666P.	Qy			
PR	26-JUL-2000; 2000US-220893P.	Db			
PR	26-JUL-2000; 2000US-220893P.	Qy			
PR	23-AUG-2000; 2000WO-US23522.	Db			
PR	24-AUG-2000; 2000WO-US23328.	Qy			
PR	15-SEP-2000; 2000US-000000P.	Db			
PR	10-NOV-2000; 2000WO-US30873.	Qy			
PR	28-NOV-2000; 2000US-253646P.	Db			
PR	01-DEC-2000; 2000WO-US32678.	Qy			
PR	20-DEC-2000; 2000US-0747259.	Db			
PR	20-DEC-2000; 2000WO-US34956.	Qy			
PR	28-FEB-2001; 2001WO-US06520.	Db			
PR	10-MAY-2001; 2001US-0854280.	Qy			
PR	25-MAY-2001; 2001WO-US17092.	Db			
PA	(GETH ) GENENTECH INC.				
XX	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;				
XX	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;				
XX	WPI; 2002-172001/22.				
XX	N-PSDB; ABK33645.				
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,				
PT	useful for treating a PRO related disorder and for diagnosing tumours				
PT	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal				
PT	tumour or liver tumour -				
XX	Claim 11; Figure 220; 359pp; English.				
XX	The invention relates to one hundred and twenty two nucleic acids				
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides				
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,				
CC	agonists and antagonists are useful for treating a PRO related disorder.				
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung				
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or				
CC	liver tumour. The PRO polypeptides are useful for stimulating the				
CC	proliferation of, or gene expression, in pericyte cells, for stimulating				
CC	the proliferation or differentiation of chondrocyte cells, for				
CC	stimulating the release of tumour necrosis factor-alpha from human blood,				
CC	for stimulating or inhibiting the proliferation of normal human dermal				
CC	fibroblast cells. The PRO polypeptide may also be used as molecular				
CC	weight markers and for tissue typing. The PRO nucleic acids have				
CC	applications in molecular biology, including use as hybridisation probes,				
CC	and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO				
CC	protein sequences of the invention.				
XX					
SQ	Sequence 417 AA;				
Query Match	100.0%; Score 2255; DB 23; Length 417;				
Best Local Similarity	99.8%; Pred. No. 2.4e-192;				
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 MALKVLLEQEKFTFTLLVGLYLSCKVTCSSGDCRQEQEFDRSGNVCPCQCGFMELSK	60			
Db	1 MALKVLLEQEKFTFTLLVGLYLSCKVTCSSGDCRQEQEFDRSGNVCPCQCGFMELSK	60			
Qy	61 ECGFGYGEDAQVTCRLRPFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG	120			
Db	61 ECGFGYGEDAQVTCRLRPFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG	120			
Qy	121 FYRKTILGVQDMCEVPCGDPPEPHCAKSNLVKVIATASSPRDTALAAVTCSSALAT	180			
Db	121 FYRKTILGVQDMCEVPCGDPPEPHCAKSNLVKVIATASSPRDTALAAVTCSSALAT	180			
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QY	61 ECGFGYGEDAQCTCRLHREKEDWGFQCKPCLDCAVNNRFQKANCATSATDAICGDCPLG 120	
DB	61 ECGFGYGEDAQCTCRLHREKEDWGFQCKPCLDCAVNNRFQKANCATSATDAICGDCPLG 120	
QY	121 FYRKTUUVGQDMCEVPCGPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180	
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QY	181 VLLALLILCVYKQPMCKEKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240	
DB	181 VLLALLILCVYKQPMCKEKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240	
QY	241 SVQTCGVRLLPSCCCEACSPNATLGCYVHSAASLOARNAGPAGEVMTFFGSLTQSI 300	
DB	241 SVQTCGVRLLPSCCCEACSPNATLGCYVHSAASLOARNAGPAGEVMTFFGSLTQSI 300	
QY	301 CGEFSDAWPLMONGMDNISFCDSYPELTGEDIHSLNPELESSTLDSNSSODLVGGAV 360	
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KW	cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;	
KW	colon tumour; breast tumour; prostate tumour; rectal tumour;	
KW	cervical tumour; liver tumour; TNF-alpha release; arthritis;	
KW	tumour necrosis factor alpha; chondrocyte cell; bone disorder;	
KW	cartilage disorder; sports injury.	
OS	Homo sapiens.	
XX	US2003036156-A1.	
PN	20-FEB-2003.	
XX	02-JUL-2002; 2002US-0188767.	
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PR	01-DEC-1998; 98WO-US25108.	
PR	08-MAR-1999; 99WO-US05028.	
PR	14-MAY-1999; 99WO-US10733.	
PR	02-JUN-1999; 99WO-US12252.	
PR	01-SEP-1999; 99WO-US20111.	
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PR	02-DEC-1999; 99WO-US28551.	
PR	30-DEC-1999; 99WO-US31274.	
PR	05-JAN-2000; 2000WO-US00219.	
PR	18-FEB-2000; 2000WO-US04341.	
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PR 01-JUL-1998; 98US-091359P.

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PR	02-JUL-1998;	98US-091626P.	XX		
PR	02-JUL-1998;	98US-091628P.	XX		
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PR	04-JUL-1998;	98US-094006P.	KW		tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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			PR	02-MAR-2000;	2000WO-US05841.
			PR	15-MAR-2000;	2000WO-US06884.
			PR	30-MAR-2000;	2000WO-US08439.
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			PR	30-MAY-2000;	2000WO-US14941.
			PR	02-JUN-2000;	2000WO-US15264.
			PR	28-JUL-2000;	2000WO-US20710.
			PR	24-AUG-2000;	2000WO-US23328.
			PR	08-NOV-2000;	2000WO-US30952.
			PR	01-DEC-2000;	2000WO-US32678.
			PR	20-DEC-2000;	2000WO-US34956.
			PR	28-FEB-2001;	2001WO-US06520.
			PR	01-JUN-2001;	2001WO-US17800.
			PR	29-JUN-2001;	2001WO-US19692.
			PR	29-JUN-2001;	2001WO-US21066.
			PR	09-JUL-2001;	2001WO-US21735.
			PR	29-AUG-2001;	2001WO-US27099.
			PR	26-JUN-1998;	98US-0105413.
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			PR	20-DEC-2000;	2000US-0747259.
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			PR	05-JUN-2001;	2001US-0866028.
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Best Local Similarity 99.8%; Pred. No. 2.4e-192;

Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	FYRKTCLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATSTASSPRDTALAAVICSALAT	180
Db	121	FYRKTCLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATSTASSPRDTALAAVICSALAT	180
Qy	181	VLLALLILCVTYCKRQFWEKPSLSQDIQYNGSELSCFDRPOLHEYAHRACCCRRD	240
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Qy	301	CGEFSDAWPLMQNPMGDNISFCDSYBELTGEDIHSLNPELESSTLDSNSSQDLVGAV	360
Db	301	CGEFSDAWPLMQNPMGDNISFCDSYBELTGEDIHSLNPELESSTLDSNSSQDLVGAV	360
Qy	361	PVQSHSNFTAAATDLSRYNNTLVESATODALTWRSQLDQESGAIHPATQTSLOEA	417
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RESULT 12

ID ABU67642 standard; Protein; 417 AA.

XX AC ABU67642;

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18-JUL-2001; 2001US-0908827.  
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 16-AUG-2001; 2001US-0931836.  
 28-AUG-2001; 2001US-0941992.  
 04-SEP-2001; 2001US-0946374.  
 15-JAN-2002; 2002US-0052596.  
 (GETH ) GENENTECH INC.  
 Baker KP, Chen J, Deanyers L, Goddard A, Godowski PJ, Gurney AL;  
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 WPI; 2003-332039/31.  
 N-PSDB; ACA05936.  
 New secreted and transmembrane PRO polypeptides and nucleic acids,  
 useful in gene therapy, in chromosome and gene mapping, as chromosome  
 markers, in tissue typing, and in chromosome identification -  
 Claim 11; Fig 474; 706pp; English.  
 The invention discloses human nucleic acids encoding secreted and  
 transmembrane (PRO) polypeptides. Also disclosed is an antibody that  
 specifically binds to the PRO polypeptide, a method for stimulating the  
 release of tumour necrosis factor alpha (TNF-alpha) from human blood by  
 contacting the blood a PRO polypeptide, a method for stimulating the  
 proliferation or differentiation of chondrocyte cells by contacting the  
 cells with a PRO polypeptide, a method for detecting the presence of a  
 tumour in a mammal and an oligonucleotide probe derived from any of the  
 PRO nucleotide sequences. The nucleotide sequences are useful as probes,  
 in chromosome and gene mapping, in generating antisense RNA and DNA, in  
 preparing PRO polypeptides by recombinant techniques and in gene therapy  
 (e.g. for replacement of defective gene). The PRO polypeptides are useful  
 as molecular weight markers for protein electrophoresis purposes, for  
 chromosome identification, as chromosome markers, as therapeutic agents,  
 for stimulating the release of TNF-alpha from human blood, for  
 stimulating the proliferation or differentiation of chondrocytes and  
 detecting the presence of a tumour. The PRO polypeptides and nucleic  
 acids may also be used diagnostically for tissue typing. The sequences  
 presented in ABU67406-ABU67710 are the PRO polypeptides of the invention.  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 2255; DB 24; Length 417;  
 Best Local Similarity 99.8%; Pred. No. 2.4e-192;  
 Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 121 FYRKTCLVGFQDMCEVPCGPPPPPEPHCAKSNLVKIASTASSPRDTALAIVCSALAT 180  
 121 FYRKTCLVGFQDMCEVPCGPPPPPEPHCAKSNLVKIASTASSPRDTALAIVCSALAT 180  
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 301 CGFSDAWPLMQNPMGDNISFCDSYELTGEDTHSLNPELESTSLDSNSSQDLVGGAV 360

QY 361 PVQSHSENFTAATDLRYNNNTLVESASTQDALTMRSQDQSGAIHPATQTSLOEA 417  
 Db 361 PVQSHSENFTAATDLRYNNNTLVESASTQDALTMRSQDQSGAIHPATQTSLOEA 417  
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 XX AC ABU65500;  
 XX DT 16-MAY-2003 (first entry)  
 XX DE Human PRO polypeptide #237.  
 XX KW Human; PRO; cytostatic; chromosome mapping; gene mapping;  
 KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;  
 KW chondrocyte differentiation; chondrocyte proliferation; tumour.  
 XX OS Homo sapiens.  
 XX PN US2003032102-A1.  
 XX PD 13-FEB-2003.  
 XX PF 17-JUN-2002; 2002US-0173697.  
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 XX PR 01-DEC-1998; 98WO-US25108.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 XX PR 14-MAY-1999; 99WO-US10733.  
 XX PR 02-JUN-1999; 99WO-US12252.  
 XX PR 01-SEP-1999; 99WO-US20111.  
 XX PR 15-SEP-1999; 99WO-US21090.  
 XX PR 01-DEC-1999; 99WO-US28301.  
 XX PR 02-DEC-1999; 99WO-US28551.  
 XX PR 30-DEC-1999; 99WO-US31274.  
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 XX PR 09-JUL-2001; 2001WO-US21735.  
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 XX PR 29-OCT-1997; 97US-063734P.

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Query Match 100.0%; Score 2255; DB 24; Length 417;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALKVLEQEKTFLLVLLVLLGYLSCKVTCSGDCRQEQEFDNRSGNVCPCNQCQGMELSK 60
Db 1 MALKVLEQEKTFLLVLLVLLGYLSCKVTCSGDCRQEQEFDNRSGNVCPCNQCQGMELSK 60
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 Qy 181 VLLALLILCVYIKRQFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240  
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 Qy 241 SVOTCGVRLILPSCCEACSPNATILGCGVHSAASIQARNAGPAGEMVPTFFGSLTQSI 300  
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RESULT 14  
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 AC ABUS8636;  
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 DT 15-APR-2003 (first entry)  
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 DE Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach;  
 KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003027272-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 21-JUN-2002; 2002US-0176492.  
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 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99WO-US05190.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
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 PR 30-NOV-1999; 99WO-US28313.  
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 PR 02-DEC-1999; 99WO-US28551.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
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## ALIGNMENTS

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; APPLICANT: Catharine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT APPLICATION NUMBER: US/09/286,529  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 25  
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; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT APPLICATION NUMBER: US/09/286,529  
; CURRENT FILING DATE: 1999-04-05  
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; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; FILE REFERENCE: PI739R1
; CURRENT FILING DATE: 2000-04-12
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Qy 93 LDCAVNRFQKANCATSDAICGDCPLPGFYRKTCLVGFQDMCEVPCGDPPPPYEPHCASK 152
Db 62 ITCAVINRVQKNCATSNVAVGDCPLPRFYRKTTRIGLQDOECIPCTKQTPTSEVQCAFQ 121

Qy 153 VNLVKIATASSPRDTALAAVICSAATVLLALLILCVIYCKRQFME--KKPSWSLSQD 210
Db 122 LSLVEADAPTVPQEATLVALVSSLLVFTLAFGLFLFYCKQFFNRHRCQRTVTGGLAQFE 181

Qy 211 IQNGSELSCFDRPQLHEVAHRACCQCRDRSVQTCGPVRLPSMCCBEACS 261
Db 182 ADTAKESLFPVPPSKETSAESQVSENIFQTQPLNPI-----LEDDCS 225

RESULT 5
US-09-342-681C-17
; Sequence 17, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-681C-17

Query Match
Best Local Similarity 8.5%; Score 191; DB 4; Length 448;
Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;

Qy 16 LLVLLGYLSCKVTCESGDCRQOEFRDR-SGNCVPCNQCGPQMELSKECGFG-YGEDAQCV 73
Db 13 LPVLVLSLMSARAESYSGCENEYNNQTTGLCQECPPCGPGEPPYLSGCGYTKDEDYGV 72

Qy 74 TCRHRRFKEDWGFQKPCDCAVNVRFQKANC-----SATSDAICGDCPLPGFY-----RKT 125
Db 73 PCPAERFSKG-GYQICRRHKDC---EGFRATVLTTPGDMENDAECPCLPGYTMLENRPR 128

Qy 126 KLVGFDQDMCEVPCGDPPPPYEPHCASKVNLVKI-----ASTASSPRDTA-----L 170
Db 125
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1  RESULT 7
2  US-08-097-827-11
3  ; Sequence 11, Application US/08097827
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Baum, Peter
6  ; Goodwin, Ray
7  ; Fanslow, William
8  ; Gayle, Richard
9  ; TITLE OF INVENTION: Novel Cytokine which is a Ligand for
10 ;
11 ; NUMBER OF SEQUENCES: 13
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Immunex Corporation
14 ; STREET: 51 University Street
15 ; CITY: Seattle
16 ; STATE: WA
17 ; COUNTRY: USA
18 ; ZIP: 98101
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: Floppy disk
21 ; COMPUTER: IBM PC compatible
22 ; OPERATING SYSTEM: PC-DOS/MS-DOS
23 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

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	TELEPHONE: 206-587-0730
/	INFORMATION FOR SEQ ID NO: 7:
/	SEQUENCE CHARACTERISTICS:
/	LENGTH: 206 amino acids
/	TYPE: amino acid
/	TOPOLOGY: linear
/	MOLECULE TYPE: protein
/	SEQUENCE DESCRIPTION: SEQ ID NO: 7:
/	US-08-097-827-7
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Best Local Similarity 6.6%; Score 150; DB 1; Length 206;	
Matches 55; Conservative 21; Mismatches 75; Indels 32; Gaps 13	
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DB	9 TALLLLG-LTLGVTAARRLNCVKHTY--PSGHKC--CRECQFHHGMVNR--DHTRDITLCH 61
QY	74 TCRLHRFKEDWGFQCKPCLCAVVNRFO-KANCATSDAICGDCPLPGFYRKTKLVGFQD 132
DB	62 PCETGYNEAVNYDTCKCTQCNHRSGSELKQNCTPTQDTVCRCPGTQPR-----QD 114
QY	133 -----MECVPCGDPPEPYEP-----HCASKYNLVKIASTASSPRDTALAAVIC---SALA 179
DB	115 SGYKLGVDCVPC--PPGHFSPGNNOACKPWNTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171
QY	180 TVL 182
DB	172 TLL 174
RESULT 10	
US-08-494-574-7	
Sequence 7, Application US/08494574	
Patent No. 5783665	
GENERAL INFORMATION:	
APPLICANT: Baum, Peter	
APPLICANT: Goodwin, Ray	
APPLICANT: Fanslow, William	
APPLICANT: Gayle, Richard	
TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for	
NUMBER OF SEQUENCES: 13	
CORRESPONDENCE ADDRESS:	
ADDRESS: Immunex Corporation	
STREET: 51 University Street	
CITY: Seattle	
STATE: WA	
COUNTRY: USA	
ZIP: 98101	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: PatentIn Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/494,574	
FILING DATE: 22-JUN-1995	
CLASSIFICATION: 530	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US/08/097,827	
FILING DATE: 23-JUL-1993	
ATTORNEY/AGENT INFORMATION:	
NAME: Perkins, Patricia A.	
REGISTRATION NUMBER: 34,693	
REFERENCE/DOCKET NUMBER: 2806	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 206-587-0730	
INFORMATION FOR SEQ ID NO: 7:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 206 amino acids	
TYPE: amino acid	
TOPOLOGY: linear	

	APPLICATION NUMBER: US/08/097,827
/	FILING DATE: 23-JUL-1993
/	ATTORNEY/AGENT INFORMATION:
/	NAME: Perkins, Patricia A.
/	REGISTRATION NUMBER: 34,693
/	REFERENCE/DOCKET NUMBER: 2806
/	TELECOMMUNICATION INFORMATION:
/	TELEPHONE: 206-587-0730
/	INFORMATION FOR SEQ ID NO: 11:
/	SEQUENCE CHARACTERISTICS:
/	LENGTH: 438 amino acids
/	TYPE: amino acid
/	TOPOLOGY: linear
/	MOLECULE TYPE: protein
/	US-08-494-574-11
Query Match	
Best Local Similarity 7.0%; Score 159; DB 1; Length 438;	
Matches 69; Conservative 31; Mismatches 93; Indels 58; Gaps 18;	
QY	15 TLLVLLGLSKVTCSGDCRQQEPRDRSGN-CVPNCQGPGMELSKCGFGYGEDAQC 73
DB	9 TALLLLG-LTLGVTAARRLNCVKHTY--PSGHKC--CRECQFHHGMVNR--DHTRDITLCH 61
QY	74 TCRLHRFKEDWGFQCKPCLCAVVNRFO-KANCATSDAICGDCPLPGFYRKTKLVGFQD 132
DB	62 PCETGYNEAVNYDTCKCTQCNHRSGSELKQNCTPTQDTVCRCPGTQPR-----QD 114
QY	133 -----MECVPCGDPPEPYEP-----HCASKYNLVKIASTASSPRDTALAAVIC---SALA 179
DB	115 SGYKLGVDCVPC--PPGHFSPGNNOACKPWNTNCTLSGKQTRHPASDSLDAV-CEDRSLLA 171
QY	180 TVLLALLILCVIKRYQWEKKPSW---SLRSODIQNGSELCDFRQPQLHEVAHRACQ 236
DB	172 TLL-----METORPFRTTVOSTTWTSELP--STPTLVE--PRSC-- 211
QY	237 CRDSVQTGCP 247
DB	212 ---DKTHTCPP 219
RESULT 9	
US-08-097-827-7	
Sequence 7, Application US/08097827	
GENERAL INFORMATION:	
APPLICANT: Baum, Peter	
Goodwin, Ray	
Fanslow, William	
Gayle, Richard	
TITLE OF INVENTION: Novel Cytokine Which is a Ligand for	
NUMBER OF SEQUENCES: 13	
CORRESPONDENCE ADDRESS:	
ADDRESS: Immunex Corporation	
STREET: 51 University Street	
CITY: Seattle	
STATE: WA	
COUNTRY: USA	
ZIP: 98101	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: PatentIn Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/097,827	
FILING DATE: 23-Jul-1993	
CLASSIFICATION: <Unknown>	
ATTORNEY/AGENT INFORMATION:	
NAME: Perkins, Patricia A.	



Qy	64	FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVNRFO-KANC SATSDAICGDCLPQFY	123
Db	52	-DHTRDTVCHPCPGPFYNEAVNYDTCKQCTQCNRHSGSELKQNCPTTETDVC-QCRPGTQ	109
Qy	123	RKTGLVGFDMECVPCCGDP PPPYP-----HCASKNVLV-----KIASTASSPRDTALA A V I	174
Db	110	PRODSSHKLGVDCVPC--PPGHFSPGSNOACKPWNTCTL SGKQIRHPASNSLDT-----V	162
Qy	175	C---SALATVL 182	
Db	163	CEDRSLLATLL 173	
RESULT 12			
US-08-795-445A-51			
; Sequence 51, Application US/08795445A			
; Patent No. 6284485			
; GENERAL INFORMATION:			
; APPLICANT: Boyle, William J.			
; APPLICANT: Lacey, David L.			
; APPLICANT: Calzone, Frank J.			
; APPLICANT: Chang, Ming-Shi			
; TITLE OF INVENTION: OSTEOPROTEGERIN			
; NUMBER OF SEQUENCES: 53			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Amgen Inc.			
; STREET: 1840 Dehavilland Drive			
; CITY: Thousand Oaks			
; STATE: California			
; COUNTRY: USA			
; ZIP: 91320-1789			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/795,445A			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/577,788			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Winter, Robert B.			
; REFERENCE/DOCKET NUMBER: A-378			
; INFORMATION FOR SEQ ID NO: 51:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 205 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; US-08-795-445A-51			
Query Match 6.4%; Score 145; DB 3; Length 205;			
Best Local Similarity 29.8%; Pred. No. 1e-05;			
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13			
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Db	6	QQPTAFLLGLSLGTVTKLVNKVDTPVPSGH-----KC--CRECQPGHGMVSR-	51
Qy	64	FGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVNRFO-KANC SATSDAICGDCLPQFY	122
Db	52	-DHTRDTVCHPCPGPFYNEAVNYDTCKQCTQCNRHSGSELKQNCPTTETDVC-QCRPGTQ	109
Qy	123	RKTGLVGFDMECVPCCGDP PPPYP-----HCASKNVLV-----KIASTASSPRDTALA A V I	174
Db	110	PRODSSHKLGVDCVPC--PPGHFSPGSNOACKPWNTCTL SGKQIRHPASNSLDT-----V	162
Qy	175	C---SALATVL 182	

Qy	15	TLLVLGYLSCKVTCSSGDCRQQBFDRSGN-CVPCNQGPOMELSKCGFGYGDAOCV	73
Db	9	TALLLLG-LTLGTARLLNCVKHTY--PSGHKC--CRECQPGHGMVSR--DHTRDTLCH	61
Qy	74	TCRLHRFKEDWGFQKCKPCLDCAVNRFO-KANC SATSDAICGDCLPQFYRKTKLVGFQD	132
Db	62	PCTGTFNEAVNYDTCKQCTQCNRHSGSELKQNCPTTQDTCV-RCRPGTQR-----QD	114
Qy	133	-----MECVPCCGDP PPPYP-----HCASKNVLV KIASTASSPRDTALA A V I C ---SALA	179
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Qy	180	TVL 182	
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RESULT 11			
US-08-974-022-51			
; Sequence 51, Application US/08974022			
; Patent No. 6015938			
; GENERAL INFORMATION:			
; APPLICANT: Boyle, William J.			
; APPLICANT: Lacey, David L.			
; APPLICANT: Calzone, Frank J.			
; APPLICANT: Chang, Ming-Shi			
; TITLE OF INVENTION: OSTEOPROTEGERIN			
; NUMBER OF SEQUENCES: 53			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Amgen Inc.			
; STREET: 1840 Dehavilland Drive			
; CITY: Thousand Oaks			
; STATE: California			
; COUNTRY: USA			
; ZIP: 91320-1789			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
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; FILING DATE: 12-DEC-1995			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/577,788			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Winter, Robert B.			
; REFERENCE/DOCKET NUMBER: A-378			
; INFORMATION FOR SEQ ID NO: 51:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 205 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; US-08-974-022-51			
Query Match 6.4%; Score 145; DB 3; Length 205;			
Best Local Similarity 29.8%; Pred. No. 1e-05;			
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;			
Qy	9	QEKTFTLLVL-LGY---LSC-KVTCESGDCRQQBFDRSRGNVCVPCNQGPOMELSKCG	63
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Db      163 CEDRSLLATLL 173

RESULT 13
US-08-795-447A-51
; Sequence 51, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-51

Query Match      6.4%; Score 145; DB 3; Length 205;
Best Local Similarity 29.8%; Pred. No. 1e-05;
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;

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Qy      64 FGYGEDAQCVCRLHRFKEDWGPKCKPCLDCAVVRFO-KANCSATSDAICGDCPLPGFY 122
Db      52 -DHTRDVCHPCPEFGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTEDTVC-QCRPGTQ 109

Qy      123 RKTLLVGFQDMCVPCGDDPPPPYEP-----HCASKVNLV-----KIATASSPRDTALAAVI 174
Db      110 PRQDSSHKLGVDVCPG--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy      175 C---SALATVL 182
Db      163 CEDRSLLATLL 173

RESULT 14
US-08-974-186-51
; Sequence 51, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:

TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:

Query Match      6.4%; Score 145; DB 3; Length 205;
Best Local Similarity 29.8%; Pred. No. 1e-05;
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;

Qy      9 QEKTFFTLLVL-LGY---LSC-KVTCESGDCRQOEFRDRSGNVCPCNQCPGMELSKECG 63
Db      6 QQPTAFLLGLSLGVTVKLNCVKDTPSGH-----KC--CRECQPGHGMVSRG- 51

Qy      64 FGYGEDAQCVCRLHRFKEDWGPKCKPCLDCAVVRFO-KANCSATSDAICGDCPLPGFY 122
Db      52 -DHTRDVCHPCPEFGFYNEAVNYDTCKQCTQCNHRSGSELKQNCPTPTEDTVC-QCRPGTQ 109

Qy      123 RKTLLVGFQDMCVPCGDDPPPPYEP-----HCASKVNLV-----KIATASSPRDTALAAVI 174
Db      110 PRQDSSHKLGVDVCPG--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162

Qy      175 C---SALATVL 182
Db      163 CEDRSLLATLL 173

RESULT 15
US-08-795-446B-51
; Sequence 51, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
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Job time : 21 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Title: US-09-780-532a-2

Perfect score: 2256

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2255	100.0	417	12	US-10-216-163-220
4	2255	100.0	417	12	US-10-187-749-474
5	2255	100.0	417	12	US-10-194-457-474
6	2255	100.0	417	12	US-10-184-642-474
7	2255	100.0	417	12	US-10-196-747-474
8	2255	100.0	417	12	US-10-173-689-474
9	2255	100.0	417	12	US-10-173-690-474
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16	2255	100.0	417	12	US-10-174-569-474	Sequence 474, App
17	2255	100.0	417	12	US-10-174-583-474	Sequence 474, App
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21	2255	100.0	417	12	US-10-175-736-474	Sequence 474, App
22	2255	100.0	417	12	US-10-175-742-474	Sequence 474, App
23	2255	100.0	417	12	US-10-175-744-474	Sequence 474, App
24	2255	100.0	417	12	US-10-175-745-474	Sequence 474, App
25	2255	100.0	417	12	US-10-175-748-474	Sequence 474, App
26	2255	100.0	417	12	US-10-175-751-474	Sequence 474, App
27	2255	100.0	417	12	US-10-175-754-474	Sequence 474, App
28	2255	100.0	417	12	US-10-176-480-474	Sequence 474, App
29	2255	100.0	417	12	US-10-176-489-474	Sequence 474, App
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31	2255	100.0	417	12	US-10-176-755-474	Sequence 474, App
32	2255	100.0	417	12	US-10-176-759-474	Sequence 474, App
33	2255	100.0	417	12	US-10-176-920-474	Sequence 474, App
34	2255	100.0	417	12	US-10-176-922-474	Sequence 474, App
35	2255	100.0	417	12	US-10-176-924-474	Sequence 474, App
36	2255	100.0	417	12	US-10-176-984-474	Sequence 474, App
37	2255	100.0	417	12	US-10-179-508-474	Sequence 474, App
38	2255	100.0	417	12	US-10-179-512-474	Sequence 474, App
39	2255	100.0	417	12	US-10-179-515-474	Sequence 474, App
40	2255	100.0	417	12	US-10-173-702-474	Sequence 474, App
41	2255	100.0	417	12	US-10-173-703-474	Sequence 474, App
42	2255	100.0	417	12	US-10-173-704-474	Sequence 474, App
43	2255	100.0	417	12	US-10-174-574-474	Sequence 474, App
44	2255	100.0	417	12	US-10-176-486-474	Sequence 474, App
45	2255	100.0	417	12	US-10-176-490-474	Sequence 474, App

ALIGNMENTS

RESULT 1  
US-09-780-532-2  
; Sequence 2, Application US/09780532  
; Patent No. US20020068696A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Clive  
; APPLICANT: Chaudhary, Divya  
; APPLICANT: Long, Andrew  
; TITLE OF INVENTION: TRADE MOLECULES, AND USES RELATED THERETO  
; FILE REFERENCE: GNN-012CP  
; CURRENT APPLICATION NUMBER: US/09/780,532  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,922  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/182,148  
; PRIOR FILING DATE: 2000-02-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-532-2

Query Match	100.0%	Score	2256	DB	9	Length	417
Best Local Similarity	100.0%	Pred. No.	5.8e-197				
Matches	417	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Oy	1	MALKVLEQKPTFTLLVLLGYLSCKVTCESGDCRQOEPRDRSGNCVPCNQCQGMELSK	60				
Db	1	MALKVLEQKPTFTLLVLLGYLSCKVTCESGDCRQOEPRDRSGNCVPCNQCQGMELSK	60				
Oy	61	ECGFGYGEDAQVCTRLHRFKEDWGFQKPCLDCAVNNRFQKNCATSDAICGDCPLPG	120				
Db	61	ECGFGYGEDAQVCTRLHRFKEDWGFQKPCLDCAVNNRFQKNCATSDAICGDCPLPG	120				
Oy	121	FYRKTKLIVGFQDMCEVCGDPPPPYPHPKCAKVNLIKIASTASSPRDTALAATCSALAT	180				
Db	121	FYRKTKLIVGFQDMCEVCGDPPPPYPHPKCAKVNLIKIASTASSPRDTALAATCSALAT	180				

Db 121 FYRKTGLVGFQDMCEVPCGDP PPPYPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Qy 181 VLLALLILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCQRRD 240  
Db 181 VLLALLILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCQRRD 240  
Qy 241 SVQTCGVRLLPSMCCBEACSPNATLGCYVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300  
Db 241 SVQTCGVRLLPSMCCBEACSPNATLGCYVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300  
Qy 301 CGEFSDAWPLMNPMPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Db 301 CGEFSDAWPLMNPMPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Qy 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417  
Db 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

## RESULT 2

US-10-199-672-474  
; Sequence 474, Application US/10199672  
; Publication No. US20030148442A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C1  
; CURRENT APPLICATION NUMBER: US/10/199,672  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 474  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-672-474

Query Match 100.0%; Score 2255; DB 12; Length 417;  
Best Local Similarity 99.8%; Pred. No. 7.2e-197;  
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MALKVLEQEKTFFTLLVLLGLYSCKVTCSGDCRQOEFRDRSGNCVPCNQCGPMELSK 60

Db 1 MALKVLEQEKTFFTLLVLLGLYSCKVTCSGDCRQOEFRDRSGNCVPCNQCGPMELSK 60  
Qy 61 ECGFGYGEDAQCVTCRLHRRFKEDWGFQCKPCLDCAVNRFOKANCATSATSDAICGDCPLG 120  
Db 61 ECGFGYGEDAQCVTCRLHRRFKEDWGFQCKPCLDCAVNRFOKANCATSATSDAICGDCPLG 120  
Qy 121 FYRKTGLVGFQDMCEVPCGDP PPPYPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Db 121 FYRKTGLVGFQDMCEVPCGDP PPPYPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Qy 181 VLLALLILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCQRRD 240  
Db 181 VLLALLILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCQRRD 240  
Qy 241 SVQTCGVRLLPSMCCBEACSPNATLGCYVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300  
Db 241 SVQTCGVRLLPSMCCBEACSPNATLGCYVHSAASLQARNAGPAGVMVPTFFGSLTQSI 300  
Qy 301 CGEFSDAWPLMNPMPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Db 301 CGEFSDAWPLMNPMPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Qy 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417  
Db 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

## RESULT 3

US-10-216-163-220  
; Sequence 220, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 220  
; LENGTH: 417

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-220

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLLLEQSKTFTLLVLLGLYSCKVTCESGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLLLEQSKTFTLLVLLGLYSCKVTCESGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60

Qy 61 ECGFGYGEDAQCVCRLHREFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHREFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120

Qy 121 FYRKTGLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db 121 FYRKTGLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

Qy 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

Qy 241 SVQTCGVPVRLLPSCMCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGVPVRLLPSCMCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy 301 CGEFSDAWPLMQNPMGGDNISFCDSYBELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGGDNISFCDSYBELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLQEA 417
Db 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLQEA 417

RESULT 4
US-10-187-749-474
; Sequence 474, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/187,749
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/052,586
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059,263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/063,121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063,486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063,540

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-220

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLLLEQSKTFTLLVLLGLYSCKVTCESGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLLLEQSKTFTLLVLLGLYSCKVTCESGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60

Qy 61 ECGFGYGEDAQCVCRLHREFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHREFKEDMGFKCKPCLDCAVNVRFQKANCATSATSDAICGDCPLG 120

Qy 121 FYRKTGLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db 121 FYRKTGLVGFQDMCEVPCGDPDPPEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

Qy 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCRRD 240

Qy 241 SVQTCGVPVRLLPSCMCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGVPVRLLPSCMCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy 301 CGEFSDAWPLMQNPMGGDNISFCDSYBELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGGDNISFCDSYBELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLQEA 417
Db 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLQEA 417

RESULT 5
US-10-194-457-474
; Sequence 474, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C296
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/10/194,457
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/052,586
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059,263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059,266
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; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063120  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063121  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063486  
 ; PRIOR FILING DATE: 1997-10-21  
 ; PRIOR APPLICATION NUMBER: 60/063540  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063541  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063544  
 ; PRIOR FILING DATE: 1997-10-28  
 ; Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 474  
 ; LENGTH: 417  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-194-457-474

Query Match 100.0%; Score 2255; DB 12; Length 417;  
 Best Local Similarity 99.8%; Pred. No. 7.2e-197;  
 Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MALKVLEQKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQPGMELSK 60  
 Db 1 MALKVLEQKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQPGMELSK 60  
 Qy 61 ECGFGYGEDAQCVTCRLHREFKEDMGFKCKPCLDCAVVRFOKANCATSDAICGDCPLG 120  
 Db 61 ECGFGYGEDAQCVTCRLHREFKEDMGFKCKPCLDCAVVRFOKANCATSDAICGDCPLG 120  
 Qy 121 FYRKTCLVGFQDMCEVPCGDPPEPPYEPHCASKVNLVKIATSPRDTALAAVICSALAT 180  
 Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPYEPHCASKVNLVKIATSPRDTALAAVICSALAT 180  
 Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPOLHEAHRAACCCRRD 240  
 Db 181 VLLALLILCVYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPOLHEAHRAACCCRRD 240  
 Qy 241 SVQTCGPVRLPSCMCEACSPNATLGCQVHSAASIQAARNAGPAGMVPFFGSLTQSI 300  
 Db 241 SVQTCGPVRLPSCMCEACSPNATLGCQVHSAASIQAARNAGPAGMVPFFGSLTQSI 300  
 Qy 301 CGEFSDAWPLMQNPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSQDLVGGAV 360  
 Db 301 CGEFSDAWPLMQNPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSQDLVGGAV 360  
 Qy 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQLDOESGAIHPATQTSLOEA 417  
 Db 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQLDOESGAIHPATQTSLOEA 417

RESULT 6  
 US-10-184-642-474  
 ; Sequence 474, Application US/10184642  
 ; Publication No. US2003015763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194  
 ; CURRENT APPLICATION NUMBER: US/10/184,642  
 ; CURRENT FILING DATE: 2002-06-27  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 474  
 ; LENGTH: 417  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-184-642-474  
 Query Match 100.0%; Score 2255; DB 12; Length 417;  
 Best Local Similarity 99.8%; Pred. No. 7.2e-197;  
 Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MALKVLEQKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQPGMELSK 60  
 Db 1 MALKVLEQKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQPGMELSK 60  
 Qy 61 ECGFGYGEDAQCVTCRLHREFKEDMGFKCKPCLDCAVVRFOKANCATSDAICGDCPLG 120  
 Db 61 ECGFGYGEDAQCVTCRLHREFKEDMGFKCKPCLDCAVVRFOKANCATSDAICGDCPLG 120  
 Qy 121 FYRKTCLVGFQDMCEVPCGDPPEPPYEPHCASKVNLVKIATSPRDTALAAVICSALAT 180  
 Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPYEPHCASKVNLVKIATSPRDTALAAVICSALAT 180  
 Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPOLHEAHRAACCCRRD 240  
 Db 181 VLLALLILCVYCKRQFMKKPSWLSRSQDIQYNGSELSCFDRPOLHEAHRAACCCRRD 240  
 Qy 241 SVQTCGPVRLPSCMCEACSPNATLGCQVHSAASIQAARNAGPAGMVPFFGSLTQSI 300  
 Db 241 SVQTCGPVRLPSCMCEACSPNATLGCQVHSAASIQAARNAGPAGMVPFFGSLTQSI 300  
 Qy 301 CGEFSDAWPLMQNPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSQDLVGGAV 360  
 Db 301 CGEFSDAWPLMQNPMGDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSQDLVGGAV 360  
 Qy 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQLDOESGAIHPATQTSLOEA 417  
 Db 361 PVQSHSENFTAATDLRYNNLTVESASTQDALTWRSQLDOESGAIHPATQTSLOEA 417

RESULT 7  
 US-10-196-747-474  
 ; Sequence 474, Application US/10196747  
 ; Publication No. US20030162250A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C346  
 ; CURRENT APPLICATION NUMBER: US/10/196,747  
 ; CURRENT FILING DATE: 2002-07-16  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 474  
 ; LENGTH: 417  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-196-747-474



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Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60
Db      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60

Qy      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120
Db      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120

Qy      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

Qy      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240

Qy      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy      301 CGEFSDAWPLMQNPMGDDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Db      301 CGEFSDAWPLMQNPMGDDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy      361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417
Db      361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

RESULT 8
US-10-173-689-474
; Sequence 474, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-689-474

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60
Db      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60

Qy      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120
Db      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120

Qy      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

Qy      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240

Qy      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Qy      301 CGEFSDAWPLMQNPMGDDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Db      301 CGEFSDAWPLMQNPMGDDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Qy      361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417
Db      361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

RESULT 9
US-10-173-690-474
; Sequence 474, Application US/10173690
; Publication No. US20030166105A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C9
; CURRENT APPLICATION NUMBER: US/10/173,690
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-690-474

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60
Db      1 MALKVLLLEQKTFPTLLVLLGLYLSCKVTCESGDCRQEQFRDRSGNCVPCNCGPGMELSK 60

Qy      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120
Db      61 ECGFGYGEDAQCVTCLRLHFRKEDMGFKCKPCLDCAVNVNRFQKANCATSDAICGDCLPG 120

Qy      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db      121 FYRKTUWVQDMCEVPCGDPPEPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180

Qy      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db      181 VLLALLILCVYCKRQFMKKPSWLSRSDIYNGSELSCFDRPOLHEYAHRAACCCRRD 240

Qy      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db      241 SVQTCGVPVRLLPSCCCEACSPNATILCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
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Db 241 SVOTCGPVRLLPSMCCBEACSPNPATLGGVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Qy 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417  
Db 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

## RESULT 10

US-10-173-691-474  
; Sequence 474, Application US/10173691  
; Publication No. US20030166106A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C13  
; CURRENT APPLICATION NUMBER: US/10/173,691  
; CURRENT FILING DATE: 2002-06-17  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 474  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-173-691-474

Query Match 100.0%; Score 2255; DB 12; Length 417;  
Best Local Similarity 99.8%; Pred. No. 7.2e-197;  
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60  
Db 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60  
Qy 61 ECGFGYGEDAQCVTCRLHRPKEDWGFKCKPCLDCAVVRNFQKANCATSATDAICGDCPLG 120  
Db 61 ECGFGYGEDAQCVTCRLHRPKEDWGFKCKPCLDCAVVRNFQKANCATSATDAICGDCPLG 120  
Qy 121 FYRKTCLVGFQDMCEVPCGDP PPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Db 121 FYRKTCLVGFQDMCEVPCGDP PPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCQRRD 240  
Db 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCQRRD 240  
Qy 241 SVOTCGPVRLLPSMCCBEACSPNPATLGGVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
Db 241 SVOTCGPVRLLPSMCCBEACSPNPATLGGVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Qy 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417  
Db 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

## RESULT 11

US-10-173-692-474  
; Sequence 474, Application US/10173692  
; Publication No. US20030166188A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C20  
; CURRENT APPLICATION NUMBER: US/10/173,692  
; CURRENT FILING DATE: 2002-06-17  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 474  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-173-692-474

Query Match 100.0%; Score 2255; DB 12; Length 417;  
Best Local Similarity 99.8%; Pred. No. 7.2e-197;  
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60  
Db 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60  
Qy 61 ECGFGYGEDAQCVTCRLHRPKEDWGFKCKPCLDCAVVRNFQKANCATSATDAICGDCPLG 120  
Db 61 ECGFGYGEDAQCVTCRLHRPKEDWGFKCKPCLDCAVVRNFQKANCATSATDAICGDCPLG 120  
Qy 121 FYRKTCLVGFQDMCEVPCGDP PPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Db 121 FYRKTCLVGFQDMCEVPCGDP PPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180  
Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCQRRD 240  
Db 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRAACCCQRRD 240  
Qy 241 SVOTCGPVRLLPSMCCBEACSPNPATLGGVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
Db 241 SVOTCGPVRLLPSMCCBEACSPNPATLGGVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
Qy 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Db 301 CGEFSDAWPLMQNPMGMDNISFCDSYPDLTGEDIHSLNPELESSTLDSNSSQDLVGGAV 360  
Qy 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417  
Db 361 PVQSHSNFTAAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

## RESULT 12

US-10-173-694-474  
; Sequence 474, Application US/10173694  
; Publication No. US20030166107A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.

```
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C19
; CURRENT APPLICATION NUMBER: US/10/173,694
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-694-474

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQFGMELSK 60
Db 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQFGMELSK 60
Qy 61 ECGFGYGEDAQCVCRLHRFKEDWGFKCKPCLDCAVVNRFOKANCATSDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHRFKEDWGFKCKPCLDCAVVNRFOKANCATSDAICGDCPLG 120
Qy 121 FYRKTCLVGFQDMCEVPCGDPDPPEYPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPDPPEYPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQNGSELSCFDRPOLHEYAHRAACCCRRD 240
Qy 241 SVQTCGVPVRLPSPMCCEACSPNATLGCYVHSAASLOARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGVPVRLPSPMCCEACSPNATLGCYVHSAASLOARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMQNPMGDNISFCDSYPELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360
Db 301 CGEFSDAWPLMQNPMGDNISFCDSYPELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360
Qy 361 PVQSHSNFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417
Db 361 PVQSHSNFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

RESULT 13
US-10-173-698-474
; Sequence 474, Application US/10173698
; Publication No. US20030166108A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C12
; CURRENT APPLICATION NUMBER: US/10/173,698
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-698-474

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQFGMELSK 60
Db 1 MALKVLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEFDRDRSGNCVPCNQCQFGMELSK 60
Qy 61 ECGFGYGEDAQCVCRLHRFKEDWGFKCKPCLDCAVVNRFOKANCATSDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHRFKEDWGFKCKPCLDCAVVNRFOKANCATSDAICGDCPLG 120
Qy 121 FYRKTCLVGFQDMCEVPCGDPDPPEYPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPDPPEYPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQNGSELSCFDRPOLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYCKRQFMKKPSWLSRSDIQNGSELSCFDRPOLHEYAHRAACCCRRD 240
Qy 241 SVQTCGVPVRLPSPMCCEACSPNATLGCYVHSAASLOARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGVPVRLPSPMCCEACSPNATLGCYVHSAASLOARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMQNPMGDNISFCDSYPELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360
Db 301 CGEFSDAWPLMQNPMGDNISFCDSYPELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360
Qy 361 PVQSHSNFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417
Db 361 PVQSHSNFTAAATDLRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSLOEA 417

RESULT 14
US-10-173-699-474
; Sequence 474, Application US/10173699
; Publication No. US20030166109A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C8
; CURRENT APPLICATION NUMBER: US/10/173,699
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-699-474

Query Match      100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```

Qy 1 MALKVLLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEQEFRRDRSGNCVPCNQCQGMELSK 60
Db 1 MALKVLLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEQEFRRDRSGNCVPCNQCQGMELSK 60
Qy 61 ECGFGYGEDAQCVCRLHRRFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHRRFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG 120
Qy 121 FYRKTKLGVGFQDMCEVPCGDPDPPEYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTKLGVGFQDMCEVPCGDPDPPEYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Qy 241 SVQTCGPVRLLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGPVRLLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMNPMPGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSSQDLVGGAV 360
Db 301 CGEFSDAWPLMNPMPGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSSQDLVGGAV 360
Qy 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSIQA 417
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSIQA 417

```

RESULT 15

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US-10-173-707-474
; Sequence 474, Application US/10173707
; Publication No. US20030166110A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C17
; CURRENT APPLICATION NUMBER: US/10/173.707
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 474
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-707-474

```

```

Query Match 100.0%; Score 2255; DB 12; Length 417;
Best Local Similarity 99.8%; Pred. No. 7.2e-197;
Matches 416; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALKVLLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEQEFRRDRSGNCVPCNQCQGMELSK 60
Db 1 MALKVLLEQEKTFPTLLVLLGYLSCKVTCESGDCRQEQEFRRDRSGNCVPCNQCQGMELSK 60
Qy 61 ECGFGYGEDAQCVCRLHRRFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVCRLHRRFKEDWGFKCKPCLDCAVVRNRFQKANCATSATDAICGDCPLG 120
Qy 121 FYRKTKLGVGFQDMCEVPCGDPDPPEYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTKLGVGFQDMCEVPCGDPDPPEYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

```

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Qy 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Qy 241 SVQTCGPVRLLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVQTCGPVRLLLPSMCCCEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy 301 CGEFSDAWPLMNPMPGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSSQDLVGGAV 360
Db 301 CGEFSDAWPLMNPMPGMDNISFCDSYPELTGEDIHSLNPELESSTSLDSSQDLVGGAV 360
Qy 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSIQA 417
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTWRSQDQESGAIHPATQTSIQA 417

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Search completed: January 29, 2004, 21:37:37  
Job time : 41 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 29, 2004, 21:36:52 ; Search time 20 Seconds  
(without alignments)  
2005.117 Million cell updates/sec

Title: US-09-780-532A-2  
Perfect score: 2256  
Sequence: 1 MALKVLEQEKTFFTLLVLL.....LDQSGAIRHPATQTSLOEA 417  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	7.0	454	1	QGMST1
2	148	6.6	416	1	tumor necrosis fac
3	146.5	6.5	435	2	nerve growth facto
4	145	6.4	271	2	tumor necrosis fac
5	144	6.4	272	2	OX40 antigen precu
6	143	6.3	1797	2	gene ox40 protein
7	142.5	6.3	1801	1	laminin beta-2 cha
8	142	6.3	1104	1	laminin beta-2 cha
9	141.5	6.3	421	1	transcription fact
10	135	6.0	465	1	tumor necrosis fac
11	133	5.9	1650	2	nerve growth facto
12	133	5.9	4660	2	dominant autoantig
13	132.5	5.9	2813	1	gp330 protein prec
14	132	5.9	277	2	von Willebrand fac
15	132	5.9	1786	1	B-cell activation
16	130.5	5.8	1170	1	laminin beta-1 cha
17	129	5.7	326	1	thrombospondin 1 p
18	126.5	5.6	1170	1	T2 protein - myxom
19	125.5	5.6	1798	2	thrombospondin 1 p
20	125	5.5	349	2	laminin beta-2 cha
21	124.5	5.5	1193	2	G2R protein - vari
22	124	5.5	837	2	laminin B2t chain
23	124	5.5	1192	2	furin (EC 3.4.21.7
24	124	5.5	1299	2	laminin gamma 2 ch
25	123.5	5.5	965	2	furin (EC 3.4.21.7
26	123	5.5	256	2	hypothetical prote
27	123	5.5	1827	2	T-cell antigen 4-1
28	122.5	5.4	1548	2	hypothetical prote
29	122	5.4	349	2	serine proteinase
					gene G4R protein -

ALIGNMENTS

RESULT 1  
QGMST1

tumor necrosis factor receptor 1 precursor - mouse  
N;Alternate names: tumor necrosis factor receptor, 55k

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 01-Dec-2000

C;Accession: A38634; B40254; S16677; S19021; I54532; I57826

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r.

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A;Molecule type: mRNA

A;Residues: 1-454 <LEW>

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: B40254

A;Molecule type: mRNA

A;Residues: 1-454 <G02>

A;Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826

R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldman

Eur. J. Immunol. 21, 1649-1656, 1991

A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis

A;Reference number: S16677; MUID:91285014; PMID:1647956

A;Accession: S16677

A;Molecule type: mRNA

A;Residues: 1-454 <BAR>

A;Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579

R;Rothe, J.G.; Brockhaus, W.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A;Reference number: S19021; MUID:92039815; PMID:1657766

A;Accession: S19021

A;Molecule type: mRNA

A;Residues: 1-454 <ROT>

A;Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849

R;Bebo, B.F.

Immunogenetics 39, 450-451, 1994

A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1

A;Reference number: I54532; MUID:94245292; PMID:8188324

A;Accession: I54532

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-454 <RES>

A;Cross-references: GB:I26349; NID:G430732; PIDN:AAA59361.1; PID:G430733

R;Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993

A;Title: Genomic organization and promoter function of the murine tumor necrosis factor 1

A;Reference number: I57826; MUID:93156721; PMID:8381516

furin (EC 3.4.21.7  
VLDL receptor prec  
hypothetical prote  
laminin beta-1 cha  
notch4 - mouse  
laminin alpha-1 ch  
laminin alpha-1 ch  
lymphocyte activat  
gene shuttle craft  
protein C16A3.6 li  
membrane glycoprot  
laminin beta-1 cha  
tumor necrosis fac  
variant-specific s  
LDL-receptor-relat  
apoptosis-mediati

A;Accession: I57826  
A;Status: Preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-393, 'G', 395-454 <RES>  
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA0465.1; PID:g202102  
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
C;Genetics:  
A;Gene: TNFR-2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F;30-212/Domain: extracellular #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-204/Domain: NGF receptor repeat homology <NG4>  
F;213-235/Domain: transmembrane #status predicted <MEM>  
F;236-454/Domain: intracellular #status predicted <INT>  
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 157; DB 1; Length 454;  
Best Local Similarity 21.0%; Pred. No. 0.00027;  
Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

Qy 34 CRQEFDRSRNCVPCNQCQPGMELSKGCGYGEDAQCVTCRLHRRFKEDWGF-QKCKPC 92  
Db 44 CPQKGYVHSKRNISCCCTKCHKGTLYVSDCP-SPGRDVTVCREKGTGTASQNYLRQLSC 102

Qy 93 LDC-AVNNRFQKANCATSDAICG-----DCLPGFYRKTLL----- 127  
Db 103 KTCRKMSQVEISFCQADKDTVCCKENQQRYLSETHFCQVDCSPCFNGTIVIPCKETQ 162

Qy 128 -----VGF--QDMCEVCPGPPPPYEPHCASKNVLKIA-----STASPRDTALAAV 173  
Db 163 NTVNCNCHAGFLRESECVPCS-----HCKNEECWKLCPLPLANVTNPQDSGTAVL 214

Qy 174 ICSALATVLLALLLTVYCKQRMKPKSWLSRSDIQNGSLSCFDRPOLHEYAHRA 233  
Db 215 L---PLVLLGLCLSLFIFI--SLMCRYPRW-----RPEVYSII--- 248

Qy 234 CCQCRDSV---QTCG-PVRLPLSMCEBACSPNATLGCVHSAASLQARN----- 281  
Db 249 ---C-RDPVPVKEKAGKPLTPAPSPFSPGPNP-TLGFSTPGFSPVSSPISPIFG 303

Qy 282 -----AGPAGEMVPTFGS--LFQSIQCG-----EFSDAWPLMQNMGDNLISFCDSPYEL 329  
Db 304 PSNWHFPVSEVPTQADPLLYESLCSVPAPTSVQKWDSSAHPQRPDNLAILYAVV 363

Qy 330 TG 331  
Db 364 DG 365

RESULT 2  
JN0006  
nerve growth factor receptor, low affinity precursor - chicken  
N;Alternate names: NGF receptor  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A;Accession: JN0006; A60504  
R;Large, T.H.; Weiskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid  
Neuron 2, 1123-1134, 1989  
A;Title: Structure and developmental expression of the nerve growth factor receptor in b  
A;Reference number: JN0006; MUID:90166579; PMID:2560385  
A;Accession: JN0006  
A;Molecule type: mRNA  
A;Residues: 1-416 <LAR>  
A;Experimental source: embryonic chick brain  
R;Heuer, J.G.; Facemile-Nainie, S.; Wheeler, E.F.; Bothwell, M.  
Dev. Biol. 137, 287-304, 1990  
A;Title: Structure and developmental expression of the chicken NGF receptor.

A;Reference number: A60504; MUID:90152140; PMID:2154393  
A;Accession: A60504  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>  
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t;  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>  
F;21-239/Domain: extracellular #status predicted <EXT>  
F;24-57/Domain: NGF receptor repeat homology <NG1>  
F;59-100/Domain: NGF receptor repeat homology <NG2>  
F;101-139/Domain: NGF receptor repeat homology <NG3>  
F;141-181/Domain: NGF receptor repeat homology <NG4>  
F;189-237/Region: serine/threonine-rich  
F;240-261/Domain: transmembrane #status predicted <MEM>  
F;262-416/Domain: intracellular #status predicted <INT>  
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 148; DB 1; Length 416;  
Best Local Similarity 31.0%; Pred. No. 0.0012;  
Matches 58; Conservative 17; Mismatches 80; Indels 32; Gaps 11;

Qy 20 LGYLCKVTC-ESGD-----CRQEFDRD-SGNCVPCNQCQPGMELSKGCGY-----G 67  
Db 82 VGLHWSAPCVESDDAVCRAYGYFQDELGSCKECSIC-----EVGFLMFPGRDS 133

Qy 68 EDACQCVTCRLHRRFKEDWGFQKCKPCLDCAVV---NRQKANCATSDAICDGLCLPGFYRKT 125  
Db 134 QDVTCECEGTSGDEANF--VDPCLPCTICEENVMVKECTATSDAECRDLHPRWTH 191

Qy 126 -KLGVFQDMCEVCPGPPPPYEPHCASKNVLKIASTASP---RDTA--LAAVICSLA 179  
Db 192 PSLAGSDSPB--PITRDPNTEGMATTLADIVTVMGSSQPVVSRGTADNLIPVYCSILA 249

Qy 180 TVLLALL 186  
Db 250 AVVVGVLV 256

RESULT 3  
I54182  
tumor necrosis factor receptor 2-related protein - human  
C;Species: Homo sapiens (man)  
C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C;Accession: I54182  
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
A;Reference number: I54182; MUID:93252381; PMID:8486360  
A;Accession: I54182  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-435 <RES>  
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C;Genetics:  
A;Gene: GDB:LTBR  
A;Cross-references: GDB:1230195; OMIM:600979  
A;Map position: 12p13.3-12p13.1  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.5%; Score 146.5; DB 2; Length 435;  
Best Local Similarity 21.4%; Pred. No. 0.0016;  
Matches 73; Conservative 42; Mismatches 107; Indels 119; Gaps 19;

Qy 16 LVLVLLGLVLSCK-----VTCESGDCRQGE---FRDRSGNVCVPCNQCQPGMELSKGCGFG 65  
Db 18 VLGLFGLLAASQPAVPPVASENQTCRDKKEYFQHRIC--CSRCPPTGYVSAC--S 73

Qy 66 YGBDAQCVTCRLHRRFKEDWGF-----QKCKPC-----LDCAVVNRQKANCATSDAIC- 114

Db 74 RIRDTVCATCAENSYNEHWNLYTLCOLCRPCDPVMGLEETAPCTSKRKTQCRQCPMFCA 133  
Qy 115 -----GDLCPGFYRKT-K-LVGFDQMECVPC-----GPPPPYEPH--CAS 151  
Db 134 AWALECHTCELLSDCPGTETAELEDEVGKGNHCVCKAGHFQNTSSFSARCQPHTRCEN 193  
Qy 152 KVNILVKIA-----STASSPRD-----TALAAVICSALATVLLALILCVIY---- 192  
Db 194 Q-GLVEAAPGTAQSDTTCKNPLEPLPPMMSGTLMVLALLPLAFPLLATVFSIWKSHP 252  
Qy 193 --CKR--QPMKKP-----SWSLRSDIOIQYNGSELSCFPRDPQLHEVHARACQCR 238  
Db 253 SLCKKGLSLKRRPQGBGNPVGWSW-----BPPKAHPYF----- 287  
Qy 239 RDSVQTGCPVRLPLSPMCEEACSNPATLGGVHSAASLQA 279  
Db 288 PDLVQPLPI-----SGDVSFVSTGLPAAPVLEA 316  
RESULT 4  
S12783  
OX40 antigen precursor - rat  
N;Alternate names: nerve growth factor receptor homolog  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C;Accession: S12783; S08036  
R;Mallet, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A;Reference number: S12783; MUID:90214614; PMID:2157591  
A;Accession: S12783  
A;Molecule type: mRNA  
A;Residues: 1-271 <MAL>  
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C;Superfamily: CD27 antigen; NGF receptor repeat homolog  
C;Keywords: growth factor receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-271/Product: OX40 antigen #status predicted <MAT>  
F;211-235/Domain: transmembrane #status predicted <TM>  
Query Match 6.4%; Score 145; DB 2; Length 271;  
Best Local Similarity 29.8%; Pred. No. 0.0012;  
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;  
Qy 9 QEXTFTLLVL-LGV---LSC-KVTCESGDCRQCFRDRSGNCVPCNQCQPGMELSKECG 63  
Db 6 QOPTAFLLGLSLGVTVKLNCVKDTPSGH-----KC--CRECQPGHGMVSR-- 51  
Qy 64 FGYGEDAQCCTCLRLHREKEDWGFKCKPCLDCAVVRFO-KANCSATSDAICGDCPLPGFY 122  
Db 52 -DHTRDTVCHPCPGFYNEAVNYDTCKQTCNHRSGSELKQNTPTEDTVC-QCRGTQ 109  
Qy 123 RYTKLVGFQDMECVPCGDDPPPPYEP-----HCASKNVLV-----KTASTASSPRDTALA 174  
Db 110 PRODSHKLGVDCVPC--PPGHFSPGNNQACKPWTNCTLSGKQIRHPASNSLDT-----V 162  
Qy 175 C---SALATVL 182  
Db 163 CEDRSLLATLL 173  
RESULT 5  
I48700  
Gene ox40 protein - mouse  
N;Alternate names: Ox40 antigen  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C;Accession: I48700; I48334; S34377  
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;  
J. Immunol. 151, 5261-5271, 1993  
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int  
A;Reference number: I48700; MUID:94044750; PMID:8228223

A;Accession: I48700  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-272 <RES>  
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
Eur. J. Immunol. 25, 926-930, 1995  
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40  
A;Reference number: I48334; MUID:95255413; PMID:7737295  
A;Accession: I48334  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-14,'G',16-272 <RE2>  
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819  
C;Genetics:  
A;Gene: ox40  
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homolog  
Query Match 6.4%; Score 144; DB 2; Length 272;  
Best Local Similarity 29.5%; Pred. No. 0.0015;  
Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;  
Qy 15 TLVLVLLGYLSKVTCSGDCRQCFRDRSGN-CVPCNQCQPGMELSKECGFGYGEDAQCV 73  
Db 9 TALILLAL-LTLGVTTARRLNCVKHTY--PSGHKC--CRECQPGHGMVSR--DHTRDTLCH 61  
Qy 74 TCRLLHREKEDWGFKCKPCLDCAVVRFO-KANCSATSDAICGDCPLPGFYRKTCLVGFOD 132  
Db 62 PCETGPFYNEAVNYDTCKQTCNHRSGSELKQNTPTQDTVC-RCRPGTQPR-----QD 114  
Qy 133 -----MECVPCGDDPPPPYEP-----HCASKNVLVKTASTASSPRDTALA 179  
Db 115 SGYKLGVDVPC--PPGHFSPGNNQACKPWTNCTLSGKQIRHPASDSLDAV-CEDRSLLA 171  
Qy 180 TVL 182  
Db 172 TLL 174  
RESULT 6  
A55677  
laminin beta-2 chain precursor (version 1) - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 17-Mar-1999  
C;Accession: A55677  
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.B.; Kurtz, K.S.; Mattei, M.G.; Champliand, M.F.;  
Genomics 24, 243-252, 1994  
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca  
A;Reference number: A55677; MUID:95213013; PMID:7698745  
A;Accession: A55677  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1797 <WEW>  
A;Cross-references: GB:X79683  
C;Genetics:  
A;Gene: GDB:LAMB2  
A;Cross-references: GDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-467/Domain: laminin-type EGF-like homology <LE02>  
F;410-467/Domain: laminin-type EGF-like homology <LE03>  
F;470-519/Domain: laminin-type EGF-like homology <LE04>  
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;783-828/Domain: laminin-type EGF-like homology <LE06>  
F;831-874/Domain: laminin-type EGF-like homology <LE07>  
F;877-924/Domain: laminin-type EGF-like homology <LE08>  
F;927-982/Domain: laminin-type EGF-like homology <LE09>  
F;985-1034/Domain: laminin-type EGF-like homology <LE10>

F;1037-1091/Domain: laminin-type EGF-like homology <LE11>  
F;1094-1139/Domain: laminin-type EGF-like homology <LE12>  
F;1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.3%; Score 143; DB 2; Length 1797;  
Best Local Similarity 22.1%; Pred. No. 0.013;  
Matches 87; Conservative 35; Mismatches 145; Indels 126; Gaps 24;

Qy 17 LVLLGLSKVTCESGDCRQOEFRDRSGNCV-----PCNQCGMELSKCEGFCYV- 67  
Db 775 LVYNGALPCQ--CNQGSLSSECNPHGQCLCKPGVVGRRCDTCAPGY-----YGFPG 825

Qy 68 -----EDACQVTCRLHRF-----KEDWGFQKCKPCL----- 93  
Db 826 TGCQACQCSPRGALSLLCERSGQCL-CRTGAFGLRCDACORQGWGPPSCPCVNCNGHAD 884

Qy 94 DCAVNRFOKA--NC-SATSDAI CGDCLPGFYRKTKLVGFQDMECVPCGDDPP-PPYEPHC 149  
Db 985 EC--NTHTGACLCGRDLTGGEHCERCITAGFHGDPRLP--YGAQCRPCPCPEGSGQRHF 939

Qy 150 ASKYNLVKIATSPRDTALAAVICSAATVLLALLILCVYCKRQFME-KKP----- 202  
Db 940 AT-----SCHQDEYSQQIVCHCRAGY---TGLRCEACAPGQFGDPSRFGACQLC 985

Qy 203 --SWSLSRSDIQ-----YNGSELSCF-----DRPQLHEYA-----HRACQCCRDS 241  
Db 986 ECGNIDPMDPDACDPHPGQCLRLHHTGEPHCAHSPGFHQAARQSCHRCTCNLLGTN 1045

Qy 242 VQTC-----GPVRLLP--CCCEACSPN--PATLGGCVHSAASLAQARNAGP- 284  
Db 1046 PQQCSPDQCHDCDSSGQCPCLPNVQALAVDRCAPFNWLTSGHGCQPCALPSRERGPT 1105

Qy 285 ----AGEMVP--TFPGSLTQSGFSDAWPLMQ 312  
Db 1106 CNETGQCHPGAGFGGRTSCQCLHWGDPGLQ 1138

RESULT 7  
MWRTS  
laminin beta-2 chain precursor - rat  
N;Alternate names: laminin chain B3; S-laminin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 10-Dec-1999  
C;Accession: S03539  
R;Hunter, D. D.; Shah, V.; Merlie, J. P.; Sanes, J. R.  
Nature 338, 229-234, 1989  
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuro  
A;Reference number: S03539; MUID:89159410; PMID:2922051  
A;Accession: S03539  
A;Molecule type: mRNA  
A;Residues: 1-1801 <HUN>  
A;Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:  
A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-35/Domain: signal sequence #status predicted <Sig>  
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>  
F;36-285/Domain: VI <DOM6>  
F;286-555/Domain: V <DOM5>  
F;286-347/Domain: laminin-type EGF-like homology <LE01>  
F;350-410/Domain: laminin-type EGF-like homology <LE02>  
F;413-470/Domain: laminin-type EGF-like homology <LE03>  
F;473-522/Domain: laminin-type EGF-like homology <LE04>  
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;556-784/Domain: IV <DOM4>  
F;786-831/Domain: laminin-type EGF-like homology <LE06>  
F;788-1196/Domain: III <DOM3>  
F;834-877/Domain: laminin-type EGF-like homology <LE07>  
F;880-927/Domain: laminin-type EGF-like homology <LE08>  
F;930-986/Domain: laminin-type EGF-like homology <LE09>  
F;989-1038/Domain: laminin-type EGF-like homology <LE10>

F;1041-1095/Domain: laminin-type EGF-like homology <LE11>  
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>  
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>  
F;1197-1412/Domain: II <DOM2>  
F;1197-1412/Region: heptad repeats  
F;1413-1445/Domain: alpha <ALP>  
F;1446-1801/Region: heptad repeats  
F;1446-1801/Domain: I <DOM1>  
F;45-50/Disulfide bonds: #status predicted  
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p  
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.3%; Score 142.5; DB 1; Length 1801;  
Best Local Similarity 22.6%; Pred. No. 0.015;  
Matches 98; Conservative 33; Mismatches 147; Indels 155; Gaps 27;

Qy 17 LVLLGLSKVTCESGDCRQOEFRDRSGNCVPCNQCGMELSKCE-----GFG--- 65  
Db 778 LVYNGALPCQ--CDPQGSLSSECNPHGQCLCKPGVVGRRCDACATGYVYGFPGAG 830

Qy 66 -----YGEDAQVTCRLHRF-----KEDWGFQKCKCLDCAVNRNF 101  
Db 831 CQACQCSPPGALSALCEGTSGQCL-CRTGAFGLRCDHCRQGWGPPNCRPC-----VCNG 884

Qy 102 QKANCATSDAI-----CGDCLPGFYRKTKLVGFQDMECVPCGDDPP-PPYEPH 148  
Db 885 RADECDHTGACLCGRDYGGEHCERCITAGFHGDPRLPYGQ---CRPCPCPEGSGQRH 941

Qy 149 CASKYNLVKIATSPRDTALAAVICSAATVLLALLILCVYCKRQFME-KKPSWSLR 207  
Db 942 FAT-----SCHRDGYSQQIVCHCRAGY---TGLRCEACAPGFGDPSKPGRCQ 987

Qy 208 ----SODIQ-----YNGSELSCF-----RPLHEYA-----HRACQCCR 239  
Db 988 LCESGNIDPDPGADPHGTGQCLRLHHTGEPHCHGCKPGFHHQAARQSCHRCTCNLLG 1047

Qy 240 DSVQTC-----GPVRLLP--SMCCBEACSPN--PATLGGCVHSAASLAQARNA 282  
Db 1048 TDPQRCPSDLDCHCDPSTGQCPCLPHVQGLSCDR-CAPFNWLTSGRCQPCACHPSRAR 1106

Qy 283 GP-----AGEMVPTFGSLTQSGFSDAWPLMQ-----NPMGSD----- 318  
Db 1107 GPTCNFTGQCHCHAG-----FGRTSCQCLHWGDPGLQCLACDPRGIDKPKQCHR 1160

Qy 319 NISFCDSYBELTG 331  
Db 1161 STGHCSCRPGVSG 1173

RESULT 8  
I38869  
transcription factor NF1 [imported] - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 02-Sep-2000  
C;Accession: I38869  
R;Song, Z.; Krishna, S.; Thanos, D.; Strominger, J. L.; Ono, S. J.  
J. Exp. Med. 180, 1763-1774, 1994  
A;Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the  
n and functions as a transcriptional repressor.  
A;Reference number: I38869; MUID:95053707; PMID:7964459  
A;Accession: I38869  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1104 <RES>  
A;Cross-references: EMBL:U15306; NID:g563216; PIDN:AAA69517.1; PID:g563217  
C;Superfamily: RING finger homology  
F;338-398/Domain: RING finger homology <RRN>

Query Match 6.3%; Score 142; DB 2; Length 1104;  
Best Local Similarity 18.8%; Pred. No. 0.0094;  
Matches 110; Conservative 58; Mismatches 182; Indels 236; Gaps 27;

Qy 24 SKVTCESGDCRQOEFRDRSGNCVPCNQCGMELSKCE-----FGYGEDAQ----- 72



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Db 440 SCNLLCHPG-----PCPPCPAFMTKTCBGRTRHVRGQAVSVHCNPPC 484
Qy 73 ---VTCRLHRRPKEDWGOKCKPCLDCAVNRFOKANGSATS-DAICGDCLPGFYRKTKLV 128
Db 485 ENILNCGHQCAELCHGGQCPQO--IILN--QVCYCGTSRDLVZGTDV-----GKSD 534
Qy 129 GFQDMEC-----VPCGD-----PYEPHC--ASKVNLVKIATASS 164
Db 535 GFQDFSLCTKCGKDLKCGNHTCSQVHPQPCQCPRLPQLVRCPCPGQTPLSQLELGSS 594
Qy 165 PRDTALAAV-----IC-SALATVLLALLILC-----VIYKROFMEKK- 201
Db 595 SRKTCMDPVPSCGKPLCGSLDFIHTCEKLCHEGDCGVPVGRTSVISCRCSFRTKEL 654
Qy 202 PSWLSRQDI-----QYNGSELSCFDRPQ-----LH--EYA 230
Db 655 PCTSLKSEDAFMCDKRCNKKRLGRIKCNICCVCKEHLKPLNCGRLKGLRCHREPC 714
Qy 231 HRACQ--CRDSVQT---CGVRLPLSMCC-----EE 258
Db 715 HRGNCQTCWQASFBELTCHCGASVYPPVPGTRPCTQTCARVHECDHPVHSHSEE 774
Qy 259 ACS-----PNPATLCGGVHSAASL----- 277
Db 775 KCPPCTFLTQKCMGKHEFRSNIPLHLVDISGLPLPCSATPLCGMHKQRLCHKGECLVDE 834
Qy 278 -----QAR-----NAGPAGEMVPTFFGLTQSI 300
Db 835 CKQPTTPTRADCGHPCHAPCHTSPCVVTACKAVELQCEGRRKEMVISEASSTYQR 894
Qy 301 CGEFSDAWPLNQNMGMGNISFCDSYBELTGEDIHSLNPELESSTLSDNSSQDLVGAV 360
Db 895 IAAISMASKITDMQLGSS-----VSIKSLITKVEHQARLECECSALERKKR--LAEAF 948
Qy 361 PVQSHSENFTATDLRSNNVLVSASTQDALTWRSQDLQDSGAI 406
Db 949 HISEDSPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 992

RESULT 9
QORT1
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Hammer, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HM>
A;Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 141.5; DB 1; Length 461;
Best Local Similarity 21.6%; Pred. No. 0.004;
Matches 72; Conservative 37; Mismatches 113; Indels 111; Gaps 20;

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Qy 34 CROQEFDRSGNVCPCNQCQGMELSKCEGFGYGEDAQCVTCRLHRRFKEDWGOKCKPCL 93
Db 44 CPQKYAHPKNNISCTCKCHKGYLVSDCP-SPQOETVCEVCDKGTFTASQ--NHVRQCL 100
Qy 94 DCAVNR--FQK--ANCSATSDAICGDCCLPGFYRKTKLVGFQDMECVPC----- 138
Db 101 SKCTCKEMFQVREISPCADMDTVCGCKKQFORLYLSETHFQCVCDCPCFNGVTIPCKE 160
Qy 139 -----GPPPPPYEPHCASKVNLVKI-----ASTASSPRDTALAAVICSALA 179
Db 161 KQNTVNCCHAGFPFLSGNECTPCS-HCKNQECHKLCPLPPVANVTNPQDSGTAVLLPLVIF 219
Qy 180 TVLLALLILCV-IYCKRQFMKKPSWSLSRQDIQYNGSELSCFDRPQLHGYAHRAQCQR 238
Db 220 LGLCLLFFICISLLC-----RYPQM-----RPRVYSII-----C- 248
Qy 239 RDSVQTCGPVR-----LLPSMCCBEACSPNPA---TLCCGV-----HSAASLQA 279
Db 249 RDS-----APVKEVEGEGIVTKPLTPASI--PAFSPNFGFNPTLGFSTTPRFSPVSTPTI 302
Qy 280 RNA-GPAG-----EMVPT-----FRGSL 296
Db 303 SPVFGPSNWHNFVPPVREVVTQCADPLLYGSL 335

RESULT 10
A26431
Nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M. J.; Misko, T. P.; Hau, C.; Herzenberg, L. A.; Shooter, E. M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.0%; Score 135; DB 1; Length 425;
Best Local Similarity 20.5%; Pred. No. 0.011;
Matches 84; Conservative 53; Mismatches 172; Indels 100; Gaps 20;
Qy 16 LLVLLGYLS--CKVTCESGDCRQOEFDRSGNVCPCNQCQGMELSKCEGFGYGEDAQCV 73

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Db 18 LLLILGVSSGAKETCSG-----LYTHSGEC--CRACNLGEGVAQPCG---ANQTVCE 66
Qy 74 TCRLLHRFKED--WGFQKCKPCLDCAVNVRFKANCSTSDAI CDCLPGFVRKTK-----126
Db 67 PCLDNVTFSDVVSATEPCCKPCTECLGL--QSMSAPCVCEADAVC--RCAYGYQDBETGHC 124
Qy 127 -----LVGFQDMCEVPCGDPDPPEPHCHCASKVNLVKIASTASSPRDTALAIVC 175
Db 125 ACSVCEVSGLVFSCQDKQNTVCBEP---EGTVSDEANHV-----DPCLPCTVC 171
Qy 176 SALATVLLALLILCVIYKROFMKKPSWSLRSQDIQVNGSELSCFDRPQLHEVRAHACC 235
Db 172 EDTERQLRE---CTPWADAECBEIPGRWIPRSTPPGSDSTAPSTQPEVPP-----220
Qy 236 QCRDSDVQTCGPVRLPSMCMCEEACSNPATLGCVHSAASLQARNAGPAGEMVPTFFGS 295
Db 221 --EQD-----LVPSTVADMVTT---VMG-----SSQPVVTRGTTDLNLPVYCSI 259
Qy 296 LTQSIGCEFS---DAMPLMNPMPGNDISFCDSYBELTGEDIHSLNPELESSTLSDNS 351
Db 260 LAAVVGLUVIAYIAFRWNSCKQKQGANRSRPNVTPPPEGEKLS-----DSGLSVDSQS 314
Qy 352 SQDLVGGAVPVQSHSENFATATDLSRYNNTLVESASTQDALTMRSOLDQ 400
Db 315 LHD-----QQHTQ---TASGQALKDGNLYSSL-----PLTKREEVEK 350

RESULT 11
S53457
dominant autoantigen gp 330 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C:Accession: S53457
R:Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A:Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of acti
A:Reference number: S53457; MUID:95151000; PMID:7848267
A:Accession: S53457
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1650 <OK>
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F:29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:72-106/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F:111-147/Domain: EGF homology <EG1>
F:153-188/Domain: EGF homology <EG2>
F:196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
F:236-278/Domain: LDL receptor WYTD-containing repeat homology <YW02>
F:279-329/Domain: LDL receptor WYTD-containing repeat homology <YW03>
F:330-373/Domain: LDL receptor WYTD-containing repeat homology <YW04>
F:374-414/Domain: LDL receptor WYTD-containing repeat homology <YW05>
F:415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F:466-505/Domain: EGF homology <EG3>
F:509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:550-586/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F:595-631/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:636-672/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:679-715/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F:720-755/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:760-794/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:799-833/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F:843-879/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F:929-963/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F:971-1006/Domain: EGF homology <EG4>
F:1012-1048/Domain: EGF homology <EG5>
F:1055-1099/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW07>
F:1100-1154/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW08>
F:1155-1188/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW09>
F:1189-1232/Domain: LDL receptor WYTD-containing repeat homology <YW10>
F:1234-1273/Domain: LDL receptor WYTD-containing repeat homology <YW11>
F:1274-1316/Domain: LDL receptor WYTD-containing repeat homology <YW12>

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F:1326-1359/Domain: EGF homology <EG6>

Query Match 5.9%; Score 133; DB 2; Length 1650;
Best Local Similarity 23.1%; Pred. No. 0.07;
Matches 97; Conservative 45; Mismatches 144; Indels 134; Gaps 30;

Qy 29 CESGDCRQOEFRDRSGNVCPCN--QCQGMELSKCEGFGYGEDA--QCQVT-----74
Db 631 CASRTCRPGQFKNGRCIPQSWKC-----DVDNDG--DYSDEPIDECTTAAYNCNDNHTF 685
Qy 75 -CRL-HRFKEDW---GFKCKPCLD-----CAVNVRFKAN-----CSATSD 111
Db 686 SKTNYRCIPQWAVCVNGFDDCRENSDEQGESVPCPSGDFRCANHHICPLRWKCDCTDD 745
Qy 112 AICGD-----CLPGFVRKTKLVGFQ--DMECVP-----CGD-----P 141
Db 746 --CGDSDNEENCVP---RECSESEFRCAQOQCIPSRWVCQDNDGSDNSDERCEMKTCH 800
Qy 142 PPVE---PHCASKVNLVKIASTASSPRDTALAIVCSAL-----ATVLLALLILCVIY 192
Db 801 PEHQCTSGHCVPK-----ALACDGRADCLDASDESACPTFPNGTYCPAAMFECKNH 853
Qy 193 -CKRQFMKKPSLSRSQDIQYNGSELS---CF---DRPOLHE-----YAHRAACCQ 237
Db 854 VCIOSF-----WICDGENCDVDSDEEHLFCFNIPCESQPRFRCDNSRCVYGHQLC---904
Qy 238 RRDVQTCGPVRLPSMCMCEEACSNPATLGCVHSAASLQARNAGPAGEMVPTFFGSLT 297
Db 905 --NGVDDCGD---GSDEKEEHCRC-KPTHKPC---TDTEYKCSN---GNCISQHYVCDN 950
Qy 298 QSTCGEFS--AWPLMNPMPGNDISFCDSYBELTGEDIHSLNPELESSTLSDNSQDL 355
Db 951 VNDGDLSDTGTGNGLDNRCAENICEQNTQLSSGFGFICSCRPGFKPSTIS-DKNSQDI 1009

RESULT 12
T42737
gp330 protein precursor - rat
N:Alternate names: megalin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42737
R:Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 9725-9729, 1994
A:Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of t
A:Reference number: A58173; MUID:95024033; PMID:7937880
A:Accession: T42737
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4660 <SAI>
A:Cross-references: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A:Experimental source: strain Sprague-Dawley; kidney
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-4660/Product: gp330 protein #status predicted <MAT>

Query Match 5.9%; Score 133; DB 2; Length 4660;
Best Local Similarity 23.1%; Pred. No. 0.21;
Matches 97; Conservative 45; Mismatches 144; Indels 134; Gaps 30;

Qy 29 CESGDCRQOEFRDRSGNVCPCN--QCQGMELSKCEGFGYGEDA--QCQVT-----74
Db 3632 CASRTCRPGQFKNGRCIPQSWKC-----DVDNDG--DYSDEPIDECTTAAYNCNDNHTF 3686
Qy 75 -CRL-HRFKEDW---GFKCKPCLD-----CAVNVRFKAN-----CSATSD 111
Db 3687 SKTNYRCIPQWAVCVNGFDDCRENSDEQGESVPCPSGDFRCANHHICPLRWKCDCTDD 3746
Qy 112 AICGD-----CLPGFVRKTKLVGFQ--DMECVP-----CGD-----P 141
Db 3747 --CGDSDNEENCVP---RECSESEFRCAQOQCIPSRWVCQDNDGSDNSDERCEMKTCH 3801
Qy 142 PPVE---PHCASKVNLVKIASTASSPRDTALAIVCSAL-----ATVLLALLILCVIY 192

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Db 3802 PEHFQCTSGHCVPK-----ALACDGRADCLDASDESACPTFPNGTYCFAAMFECKNH 3854  
Qy 193 -CKQPMKKPSWLSRSDIQVNGSELS---CF-----DRPOLHE-----YAHRAACQC 237  
Db 3855 VCISGF-----WICDGENCDVGSDEBIHLCPNIPCESPQFRCDNSRCVYHQLC--- 3905  
Qy 238 RRDVSQTCGPVRLFLPSCMCCEACSPNPATLGGVHSAASLQARNAGPAGEMVPTFFGSLT 297  
Db 3906 --NGVDDCGD---GSDEKEBHC-RKPTHKFC---TDTEYKCSN---GNCISQHYVCDN 3951  
Qy 298 QSICGEFSD--AWPLMQPMGCDNISFCDSVPBLTGEDIHSLNPELESSTSLDSSNQDL 355  
Db 3952 VNDCCGLSDTGTCNLGDNRTCAENICEQNTQLSSGGFICSCRFQKFPSTS-DKNSCQDI 4010

RESULT 13  
VWU  
von Willebrand factor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 04-Dec-1986 #bequence revision 30-Jun-1993 #text change 22-Jun-1999  
C:Accession: A34480; S02377; A37139; S23676; A25298; A25469; A25366; S23618; S23645; A94  
R/Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora  
J. Biol. Chem. 264, 19514-19527, 1989  
A:Title: Structure of the gene for human von Willebrand factor.  
A:Reference number: A34480; MUID:90062044; PMID:2584182  
A:Accession: A34480  
A:Molecule type: DNA  
A:Residues: 1-2813 <MAN>  
A:Cross-references: EMBL:M25864  
R/Bonthron, D.; Orkin, S.H.  
Eur. J. Biochem. 171, 51-57, 1988  
A:Title: The human von Willebrand factor gene. Structure of the 5' region.  
A:Reference number: S02377; MUID:88111704; PMID:2828057  
A:Accession: S02377  
A:Molecule type: DNA  
A:Residues: 1-177 <BO2>  
A:Cross-references: EMBL:X06828  
R/Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora  
Biochemistry 30, 253-269, 1991  
A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and differ  
A:Reference number: A37139; MUID:91105089; PMID:1988024  
A:Accession: A37139  
A:Molecule type: DNA  
A:Residues: 990-1947 <MAD>  
A:Cross-references: GB:M60675; NID:G340357; PIDN:AAA61295.1; PID:G553810  
A:Note: the authors translated the codon CGC for residue 156 as Gln  
R/Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,  
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987  
A:Title: Molecular cloning of the human gene for von Willebrand factor and identificatio  
A:Reference number: S23676; MUID:87260814; PMID:3496594  
A:Accession: S23676  
A:Molecule type: DNA  
A:Residues: 2731-2813 <COL>  
A:Cross-references: EMBL:M16945  
R/Bonthron, D.; Orr, E.C.; Mitscock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.  
Nucleic Acids Res. 14, 7125-7127, 1986  
A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
A:Reference number: A25298; MUID:87016349; PMID:3489923  
A:Accession: A25298  
A:Molecule type: mRNA  
A:Residues: 1-470, 'V', 472-2813 <BON>  
A:Cross-references: EMBL:X04385  
R/Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.  
EMBO J. 5, 1839-1847, 1986  
A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei  
A:Reference number: A91044; MUID:87004550; PMID:3019665  
A:Accession: A25469  
A:Molecule type: mRNA  
A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
A:Cross-references: EMBL:X04146  
A:Note: this sequence has been revised in reference A91056  
R/Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.

EMBO J. 5, 3074, 1986  
A:Reference number: A91056  
A:Accession: A25366  
A:Molecule type: mRNA  
A:Residues: 1021-1030 <VE2>  
A:Note: this is a revision to the sequence from reference A91044  
R/Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletiich, J.P.; Sadler, J.E.  
Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated  
A:Reference number: S23618; MUID:87213253; PMID:3495266  
A:Accession: S23618  
A:Molecule type: mRNA  
A:Residues: 1-120 <SH2>  
A:Cross-references: EMBL:M17588; NID:G799330; PIDN:AAA65940.1; PID:G340316  
A:Accession: S23645  
A:Molecule type: protein  
A:Residues: 23-56 <SH3>  
R/Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand facto  
A:Reference number: A94060; MUID:86016708; PMID:2864688  
A:Accession: A94060  
A:Molecule type: mRNA  
A:Residues: 'WA', 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873; 1289-1471, 'D', 1473-  
A:Note: the authors translated the codon TCG for residue 2168 as Cys  
R/Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.  
Biochemistry 25, 3164-3171, 1986  
A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc  
A:Reference number: A90504; MUID:86269894; PMID:3488076  
A:Accession: A90504  
A:Molecule type: mRNA  
A:Residues: 781-788, 'A', 790-1424 <SHE>  
A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found  
R/Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; O  
Science 228, 1401-1406, 1985  
A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones  
A:Reference number: A44178; MUID:85244588; PMID:3874428  
A:Accession: A44178  
A:Molecule type: mRNA  
A:Residues: 2821-2813 <GIN>  
A:Cross-references: EMBL:X03028; NID:G340308; PIDN:AAA61293.1; PID:G340309  
R/Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; v  
Nucleic Acids Res. 13, 4699-4717, 1985  
A:Title: Construction of cDNA coding for human von Willebrand factor using antibody prob  
A:Reference number: S07363; MUID:85269603; PMID:3875078  
A:Accession: S07363  
A:Molecule type: mRNA  
A:Residues: 2731-2813 <VE3>  
A:Cross-references: EMBL:X02672; NID:G37939; PIDN:CAA26503.1; PID:G37940  
R/Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livin  
Cell 41, 49-56, 1985  
A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a  
A:Reference number: S23678; MUID:85201687; PMID:3873280  
A:Accession: S23678  
A:Molecule type: mRNA  
A:Residues: 2731-2813 <LYN>  
A:Cross-references: EMBL:X03028  
R/Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;  
Biochemistry 25, 3171-3184, 1986  
A:Title: Amino acid sequences of human von Willebrand factor.  
A:Reference number: A90505; MUID:86269895; PMID:3524673  
A:Accession: A90505  
A:Molecule type: protein  
A:Residues: 784-788, 'A', 790-1471, 'D', 1473-2813 <TIT>  
A:Note: 789-Thr was also found  
R/Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.  
Biochemistry 25, 3146-3155, 1986  
A:Title: Human von Willebrand factor: a multivalent protein composed of identical subuni  
A:Reference number: A23464; MUID:86269892; PMID:3015199  
A:Accession: A23464  
A:Molecule type: protein  
A:Residues: 764-773; 2803-2813 <CHO>  
R/Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.



A:Title: Sequence of the cDNA encoding the laminin B1 chain reveals a multidomain protein  
A:Reference number: A26413; MUID:87147212; PMID:3493487  
A:Accession: A26413  
A:Molecule type: mRNA  
A:Residues: 1-1786 <SAS>  
A:Cross-references: EMBL:M15525; NID:q198700  
A>Note: translation in GenBank has additional 48 residues at the amino end  
R:Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A:Reference number: S02678; MUID:88326259; PMID:2458101  
A:Accession: S02679  
A:Molecule type: protein  
A:Residues: 28-42;932-946 <FUJ>  
R:Hartl, L.; Oberbaeumer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A:Title: The N terminus of laminin A chain is homologous to the B chains.  
A:Reference number: S00624; MUID:8825080; PMID:3267223  
A:Accession: S05326  
A:Molecule type: protein  
A:Residues: 457-466;854-868;932-946 <HAR>  
R:Mann, K.; Deutzmann, R.; Timpl, R.  
Eur. J. Biochem. 178, 71-80, 1988  
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and the  
A:Reference number: S08895; MUID:89078415; PMID:2462498  
A:Accession: S14877  
A:Molecule type: protein  
A:Residues: 590-620 <MAN>  
R:Barlow, D.P.; Green, N.M.; Kurkinen, M.; Hogan, B.L.M.  
EMBO J. 3, 2355-2362, 1984  
A:Title: Sequencing of laminin B chain cDNAs reveals C-terminal regions of coiled-coil a  
A:Reference number: A02870; MUID:85051302; PMID:6209134  
A:Accession: A02871  
A:Molecule type: mRNA  
A:Residues: 1292-1530, 'MEMP', 1535-1691, 'C', 1693-1748, 'N', 1750-1786 <BAR>  
A:Cross-references: EMBL:X05212; NID:952861; PIDN:CAA28839.1; PID:9809042  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te  
A:Reference number: S01790; MUID:89030693; PMID:3181157  
A:Accession: S02036  
A:Molecule type: protein  
A:Residues: 1561-1587 <DEU>  
R:Paulsson, M.; Deutzmann, R.; Timpl, R.; Dalzoppo, D.; Odermatt, E.; Engel, J.  
EMBO J. 4, 309-316, 1985  
A:Title: Evidence for coiled-coil alpha-helical regions in the long arm of laminin.  
A:Reference number: S13543; MUID:85257455; PMID:3848400  
A:Accession: S13543  
A:Molecule type: protein  
A:Residues: 1700-1748, 'N', 1750-1759 <PAU>  
C:Genetics:  
A:Gene: Lamb-1  
A:Map position: 12  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: interact with cells and with other basement membrane proteins to promote  
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-1786/Product: laminin beta-1 chain #status predicted <MAT>  
F:22-270/Domain: VI <DOM6>  
F:271-540/Domain: V <DOM5>  
F:271-332/Domain: laminin-type EGF-like homology <LE01>  
F:335-395/Domain: laminin-type EGF-like homology <LE02>  
F:398-455/Domain: laminin-type EGF-like homology <LE03>  
F:458-507/Domain: laminin-type EGF-like homology <LE04>  
F:510-540/Domain: laminin-type EGF-like homology <LE05>  
F:541-772/Domain: IV <DOM4>  
F:773-1182/Domain: III <DOM3>  
F:773-818/Domain: laminin-type EGF-like homology <LE06>  
F:821-864/Domain: laminin-type EGF-like homology <LE07>  
F:867-914/Domain: laminin-type EGF-like homology <LE08>  
F:917-973/Domain: laminin-type EGF-like homology <LE09>

F:976-1025/Domain: laminin-type EGF-like homology <LE10>  
F:1028-1081/Domain: laminin-type EGF-like homology <LE11>  
F:1084-1129/Domain: laminin-type EGF-like homology <LE12>  
F:1132-1176/Domain: laminin-type EGF-like homology <LE13>  
F:1183-1397/Domain: II <DOM2>  
F:1183-1397/Region: heptad repeats  
F:1398-1430/Domain: alpha <ALP>  
F:1431-1786/Region: heptad repeats  
F:1431-1786/Domain: I <DOM1>  
F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:30-35/Disulfide bonds: #status predicted  
F:120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydrate  
F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 5.9%; Score 132; DB 1; Length 1786;  
Best Local Similarity 20.6%; Pred. No. 0.09;  
Matches 83; Conservative 32; Mismatches 125; Indels 162; Gaps 24;

Qy	21	GYLSCKVTCSGDCRQOEFRDRSGNCVY-----CNQCGPMELSKCEGFGYGED-----	69
Db	779	GSLSSVCDPNGGQCQ-----CRPNVVGRTCNRCAPT-----FGFGNGCKPC	821
Qy	70	-----AQCVTCLHRPK-----EDWGFQKCKPC-----LDCAVNR	100
Db	822	DCHLQGSASAFCDAITQCCHCFQGIYARQCDCRCLPGYMGFPSCQPCQCGNCHALDCTVT-	880
Qy	101	FORKANCATSDAI-----CGDCLPGFYRKTKLVGFQDMCEVCPCGPPPP-----YEPHCAS	151
Db	881	---GECUSQDYTTGHNCCERCLAGY-GDPIIGSGD-HCRPCPCPDGDSGRQARSQY	935
Qy	152	KVNLVKIASTASSPRDTALAAVTCSSALATVLLALLILCVYCKRQFMKKFWSLSRSDI	211
Db	936	DPVTQLQACVC---DPGYIGSRCDD-----CASGFFGNPSDFGSGCQPC	976
Qy	212	QYN-----GSELSCF-----DRPOLHEYAH-----RAC-----	234
Db	977	QCHHNIDTTDPEACDKDTGRCLKLYHTEGDHCOLCOYGYGADALRODCRCKVCVNYLGTV	1036
Qy	235	-----COCRRDSVO-TCGPVRLLPSCCEEACSPNATL-----CGVHSAASLQARN	281
Db	1037	KEHNGSDCHCDKATGQCSCLP-NVIGQNC--DKCAPNTWQLASGTGCGPCNCNA--AHS	1091
Qy	282	AGPAGENVPTFFGSLTOSICGEFSDAWPLMQNPNGGDNIISFC	323
Db	1092	FGPS-----CNEFTGCQCMPG-FGGRTCSEC	1117

Search completed: January 29, 2004, 21:40:33  
Job time : 22 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 29, 2004, 21:33:06 ; Search time 18 seconds  
(without alignments)

1089.452 Million cell updates/sec

Title: US-09-780-532A-2

Perfect score: 2256

Sequence: 1 MALKVLEQKEFTFLVLL.....LDQSGAIHPATQTSIQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2246	99.6	423	1	TR19_HUMAN
2	1565.5	69.4	416	1	TR19_MOUSE
3	480.5	21.3	297	1	XEDA_HUMAN
4	198	8.8	448	1	EDAR_MOUSE
5	191	8.5	448	1	EDAR_HUMAN
6	185	8.2	514	1	EDAR_ORYLA
7	157	7.0	454	1	TR1A_MOUSE
8	148	6.6	416	1	TR16_CHICK
9	146.5	6.5	435	1	TNR3_HUMAN
10	145	6.4	271	1	TNR4_RAT
11	144	6.4	272	1	TNR4_MOUSE
12	142.5	6.3	1801	1	LMB2_RAT
13	142	6.3	1104	1	NFX1_HUMAN
14	141.5	6.3	461	1	TR1A_RAT
15	141	6.2	430	1	TR1T_MACPA
16	138	6.1	417	1	TR16_MOUSE
17	136.5	6.1	430	1	TR1T_HUMAN
18	135	6.0	425	1	TR16_RAT
19	134.5	6.0	415	1	TNR3_MOUSE
20	133	5.9	625	1	TR11_MOUSE
21	133	5.9	4660	1	LRP2_RAT
22	132.5	5.9	1798	1	LMB2_HUMAN
23	132.5	5.9	2813	1	VNF_HUMAN
24	132	5.9	176	1	TR23_MOUSE
25	132	5.9	277	1	TNR5_HUMAN
26	132	5.9	1786	1	LMB1_MOUSE
27	131.5	5.8	1799	1	LMB2_MOUSE
28	130.5	5.8	1170	1	TSP1_MOUSE
29	129	5.7	326	1	V72_KXVL
30	126.5	5.6	470	1	TR1A_BOVIN
31	126.5	5.6	1170	1	TSP1_HUMAN
32	125.5	5.6	1696	1	PCK5_BRACL
33	124.5	5.5	1587	1	LMG3_HUMAN

34	124	5.5	1170	1	TSP1_BOVIN
35	123.5	5.5	830	1	SREC_HUMAN
36	123.5	5.5	965	1	YNC3_YEAST
37	123.5	5.5	1173	1	TSP1_XENLA
38	123	5.5	256	1	TNR9_MOUSE
39	122.5	5.4	1877	1	PCK5_MOUSE
40	122	5.4	349	1	CRMB_VARV
41	122	5.4	1679	1	FUR2_DROME
42	121.5	5.4	863	1	LDVR_CHICK
43	121.5	5.4	3695	1	LMAS_HUMAN
44	121	5.4	1786	1	LMB1_HUMAN
45	121	5.4	1964	1	NTC4_MOUSE

## ALIGNMENTS

RESULT 1  
ID TR19\_HUMAN  
AC Q9NS68; Q9BX29; Q9BY00; Q9NZV2; STANDARD; PRT; 423 AA.  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 19 precursor  
DE (Toxicity and JNK inducer) (TRADE).  
GN TNFRSF19 OR TROY OR TAJ.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2;  
RP TRAF3 AND TRAF5.  
RC TISSUE=fetal spleen;  
RX MEDLINE=20270246; PubMed=10809768;  
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;  
RT "TAJ, a novel member of the tumor necrosis factor receptor family,  
RT activates the c-Jun N-terminal kinase pathway and mediates  
RT caspase-independent cell death.";  
RL J. Biol. Chem. 275:15336-15342(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Glial tumor;  
RX MEDLINE=20347167; PubMed=10764796;  
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA Senba E., Kitamura T.;  
RT "TROY, a newly identified member of the tumor necrosis factor receptor  
RT superfamily, exhibits a homology with Edar and is expressed in  
RT embryonic skin and hair follicles.";  
RL J. Biol. Chem. 275:20742-20747(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Chaudhary D., Long A.J.;  
RT "TRADE, a novel TNF receptor family member associated with death  
RT signaling.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Can mediate activation of JNK and NF-kappa-B. May  
CC promote caspase-independent cell death.  
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=TAJ-alpha, TRADEalpha;  
CC IsoId=Q9NS68-1; Sequence=Displayed;  
CC Name=2; Synonyms=TRADEbeta;  
CC IsoId=Q9NS68-2; Sequence=VSP\_006512;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Highly expressed in prostate. Detected at  
CC lower levels in thymus, spleen, testis, uterus, small intestine,  
CC colon and peripheral blood leukocytes.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -----

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EMBL; AF167555; AAF71828.1; --  
 EMBL; AF040434; BAB03269.1; --  
 EMBL; AF246998; AAK28395.1; --  
 EMBL; AF246999; AAK28396.1; --  
 Genew; HGNC:11915; TNFRSF19.  
 MIM; 606122; --  
 GO; GO:0016021; C: integral to membrane; NAS.  
 GO; GO:0005031; P: tumor necrosis factor receptor activity; NAS.  
 GO; GO:0006917; P: induction of apoptosis; NAS.  
 GO; GO:0007254; P: JNK cascade; NAS.  
 InterPro; IPR001368; TNFR\_c6.  
 Pfam; PF00020; TNFR\_c6; 2.  
 SMART; SM00208; TNFR; 2.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
 Alternative splicing.  
 SIGNAL 1 29  
 CHAIN 30 423  
 DOMAIN 30 170  
 TRANSMEM 171 191  
 DOMAIN 192 423  
 REPEAT 33 72  
 REPEAT 74 114  
 REPEAT 116 149  
 REPEAT 34 46  
 DISULFID 49 62  
 DISULFID 52 72  
 DISULFID 75 89  
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 DISULFID 95 114  
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 CARBOHYD 105 105  
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 CONFLICT 405 405  
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 Best Local Similarity 99.8%; Pred. No. 3e-163;  
 Matches 414; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALKVLEQETPTLLVLLGYLSCKVTCESGDCRQEQFRDRSGNCVPCNQCQGMELSK 60  
 DB 1 MALKVLEQETPTLLVLLGYLSCKVTCESGDCRQEQFRDRSGNCVPCNQCQGMELSK 60  
 QY 61 ECGFGYGEDAQVTCRLRFPKEDMGFKCPCLDCAVNVNRFQKNCATSATSDAICGDCPLG 120  
 DB 61 ECGFGYGEDAQVTCRLRFPKEDMGFKCPCLDCAVNVNRFQKNCATSATSDAICGDCPLG 120  
 QY 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCAKSNLVKVIKASTASSPRDTALAIVCSALAT 180  
 DB 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCAKSNLVKVIKASTASSPRDTALAIVCSALAT 180  
 QY 181 VLLALLILCVTYCKRQPMKEKPSLSRSDIOYNGSELSCFDRPOLHEYAHRACCCRRD 240  
 DB 181 VLLALLILCVTYCKRQPMKEKPSLSRSDIOYNGSELSCFDRPOLHEYAHRACCCRRD 240

QY 241 SVTCGCPVRLLPSCMCCEACSPNPATLGCQVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
 DB 241 SVTCGCPVRLLPSCMCCEACSPNPATLGCQVHSAASLQARNAGPAGMVPTFFGSLTQSI 300  
 QY 301 CGFSDAWPLMQNPMGDDNIFCDSPYELTGEDIHSLNPELSESTSLDSSQDLVGGAV 360  
 DB 301 CGFSDAWPLMQNPMGDDNIFCDSPYELTGEDIHSLNPELSESTSLDSSQDLVGGAV 360  
 QY 361 PVQSHSENFTAATDLGRYNNLTVESASTQDALMRSQDOESGAIHPATQTSIQ 415  
 DB 361 PVQSHSENFTAATDLGRYNNLTVESASTQDALMRSQDOESGAIHPATQTSIQ 415  
 RESULT 2  
 TR19 MOUSE  
 ID TR19 MOUSE STANDARD; PRT; 416 AA.  
 AC Q9JLL3; Q9JHF1; Q9JH6; Q9JLL2; Q9QXW7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 19 precursor  
 DE (Toxicity and JNK inducer) (TRADE).  
 GN TNFRSF19 OR TROY OR TAJ.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=20054362; PubMed=10585776;  
 RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;  
 RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor  
 RL receptor superfamily,";  
 RN Genomics 62:103-107(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX TISSUE=Embryo, and Spleen;  
 RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;  
 RT "TAJ, a novel member of the tumor necrosis factor receptor family,  
 RT activates the c-Jun N-terminal kinase pathway and mediates  
 RT caspase-independent cell death,";  
 RN J. Biol. Chem. 275:15336-15342(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
 RX TISSUE=Brain;  
 RA MEDLINE=20347167; PubMed=10764796;  
 RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Senba E., Kitamura T.;  
 RT "TROY, a newly identified member of the tumor necrosis factor receptor  
 RT superfamily, exhibits a homology with Edar and is expressed in  
 RT embryonic skin and hair follicles,";  
 RN J. Biol. Chem. 275:20742-20747(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX STRAIN=C57BL/6;  
 RA Chaudhary D., Long A.J.;  
 RT "TRADE, a novel TNF receptor family member associated with death  
 RT signaling,";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Can mediate activation of c-Jun and NF-kappa-B. May  
 CC promote caspase-independent cell death (By similarity). Isoform 2  
 CC and isoform 3 may act as decoy receptors.  
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 3 and  
 CC 4); Secreted (isoform 2) (Probable).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=TAJ-alphaL;  
 CC IsoId=Q9JLL3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=TAJ-betaL;  
 CC IsoId=Q9JLL3-2; Sequence=VSP\_006513, VSP\_006514;







transcripts are almost exclusively confined to maturing follicles and the recently initiated placodes.

-!- INDUCTION: By activin A in E12 dental epithelium.

-!- DISEASE: Defects in EDAR are a cause of the downless phenotype in mice (the equivalent of anhidrotic ectodermal dysplasia in humans). The disease is characterized by sparse hair (atrachosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.

-!- SIMILARITY: Contains 3 TNFR-Cys repeats.

-!- SIMILARITY: Contains 1 death domain.

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EMBL; AF160502; AAD50425.1; -;  
EMBL; AK004576; BAB23385.1; ALT\_INIT.  
MGD; MGI:1343498; Edar.  
InterPro; IPR000488; Death.  
InterPro; IPR001368; TNFR\_C6.  
Pfam; PF00531; Death; 1.  
PROSITE; PS50017; DEATH DOMAIN; FALSE NEG.  
PROSITE; PS00652; TNFR\_NGFR 1; FALSE NEG.  
PROSITE; PS50050; TNFR\_NGFR 2; FALSE NEG.  
Receptor; Developmental protein; Differentiation; Apoptosis;  
Disease mutation; Transmembrane; Glycoprotein; Repeat; Signal.  
SIGNAL 1 26  
CHAIN 27 448  
TUMOR NECROSIS FACTOR RECEPTOR  
SUPERFAMILY MEMBER EDAR.  
EXTRACELLULAR (POTENTIAL).  
POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
DEATH.  
TNFR-CYS 1.  
TNFR-CYS 2.  
TNFR-CYS 3.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
POTENTIAL.  
N-LINKED (GLCNAC... (POTENTIAL).  
E -> K (IN RECESSIVE DOWNLESS JACKSON).  
FCCAF38F3D6BB971 CRC64;  
448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;  
8.8k; Score 198; DB 1; Length 448;  
Best Local Similarity 28.2k; Pred. No. 8.1e-08;  
Matches 61; Conservative 32; Mismatches 83; Indels 40; Gaps 11;  
16 LLVLGLVSLKVCESGDCRQEFDR -SGNVCPCNQCQGMELSKGCFG-YGEDACV 73  
13 LPVLVSLMCAKAEDSNCGENYHNTGLCQCPCPCGPEEPVMSGCGTKDDYGCV 72  
74 TCRLLRFKEDNGFQKCPCLCAVNVNPFQKANC-----SATSDAICGDCCLPGFY----RKT 125  
73 PCPAEKFSKG-GYQICRRHKDC--EGFFRATVLTGDMENDACGCLPGGYMLENRP 128  
126 KLVGQDMECVPCGDPDPPEPHCASKVNLKIASTASSPRDTA-----L 170  
129 NIYG---MVCYSC-LLAPNPKCEVGATSGVSAHSSTSGSGTSLPFOAHKELSGQGH 184  
171 AAVICSAATLVL---LALLILCVICKRQFMKKPS 203  
185 ATALIIMSTFIWAIIVLIMFY----IMTKPS 216

RESULT 5  
EDAR\_HUMAN

EDAR\_HUMAN STANDARD; PRT; 448 AA.  
Q9UNE0; Q9UND9;  
28-FEB-2003 (Rel. 41, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
Tumor necrosis factor receptor superfamily member EDAR precursor (Anhidrotic ectodysplasia receptor 1) (Ectodysplasin-A receptor) (EDA-A1 receptor) (Ectodermal dysplasia receptor) (Downless homolog).  
EDAR OR DL.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI TaxID=9606;  
[1]  
SEQUENCE FROM N.A., AND VARIANTS HED ARG-87; HIS-89 AND GLN-420.  
TISSUE=Fetal heart, and Skin;  
MEDLINE=99364416; PubMed=10431241;  
Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A., Zonana J.;  
"Mutations in the human homologue of mouse dl cause autosomal recessive and dominant hypohidrotic ectodermal dysplasia."; Nat. Genet. 22:366-369 (1999).  
[2]  
CHARACTERIZATION OF VARIANT GLN-420, MUTAGENESIS OF GLU-379, CHARACTERIZATION, AND INTERACTION WITH TRAF1 AND TRAF3.  
MEDLINE=21264720; PubMed=11035039;  
Kumar A., Eby M.T., Sinha S., Jasmin A., Chaudhary P.M.;  
"The ectodermal dysplasia receptor activates the nuclear factor-kappaB, JNK, and cell death pathways and binds to ectodysplasin A."; J. Biol. Chem. 276:2668-2677 (2001).  
[3]  
EDA ISOFORM A1 BINDING  
MEDLINE=20495245; PubMed=11039935;  
Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A., de Vos A.M., Gao W.-Q., Dixit V.M.;  
"Two-amino acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors."; Science 290:523-527 (2000).  
RL  
-!- FUNCTION: Receptor for EDA isoform A1, but not for EDA isoform A2. Mediates the activation of NF-kappa-B and JNK. May promote caspase-independent cell death.  
CC  
-!- SUBUNIT: Binds to EDARADD. Associates with TRAF1, TRAF2, TRAF3 and NIK.  
CC  
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC  
-!- TISSUE SPECIFICITY: Detected in fetal kidney, lung, skin and cultured neonatal epidermal keratinocytes. Not detected in lymphoblast and fibroblast cell lines.  
CC  
-!- DEVELOPMENTAL STAGE: Found in craniofacial tissues from embryonic day 42-53. Expressed in fetal skin 11 and 15 weeks after gestation.  
CC  
-!- DISEASE: Defects in EDAR are a cause of autosomal recessive and dominant anhidrotic (hypohidrotic) ectodermal dysplasia (HED or EDA), a disease characterized by sparse hair (atrachosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.  
CC  
-!- SIMILARITY: Contains 1 death domain.  
CC  
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC  
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EMBL; AF130988; AAD50076.1; -;  
EMBL; AF130986; AAD50077.1; -;  
EMBL; AF130990; AAD50077.1; JOINED.  
EMBL; AF130991; AAD50077.1; JOINED.  
EMBL; AF130992; AAD50077.1; JOINED.  
EMBL; AF130993; AAD50077.1; JOINED.



Best Local Similarity	24.8%; Pred. No. 9.2e-07;	Matches	63; Conservative	37; Mismatches	82; Indels	72; Gaps	14;
QY	9 QKTF--TLLVLLGLYSKVTCSGDCRQOEFRDRSGN-CVPCNQCQPGMELSKCGFG	65					
DB	9 QKSNFLSLLVCCMFAS-----AEYSSCGEYEFNQTNSQACQFCRQEPNWSCHG	64					
QY	66 YGEDA-QCVTCRLRLPKEDWQKCKPCLDCAVNRFOKANC-----SATSDATCGDCLPG	120					
DB	65 MKDEGFACVPCPGQYKSG-KYEICRRHKDC---NALLYKATVREPGTAEDKACGCPCLPG	120					
QY	121 FYR-NTKLVGFDMECVPCGDP-----PPVEPHCASKVNLVKIAPASS	164					
DB	121 YTMLENARNLYAMVCHSCQAPLNTKECKTTTAITKPPINPGST-----VLPHPGS	174					
QY	165 PRDTALAAVICSAATLVL---LALLILCVYCKRQFMKKPSWLSRQDIYNGSELSCF	221					
DB	175 PQGCHLATALIATMSTIFMAIAVLIIMFY-----ILKAKE-----NG-----	213					
QY	222 DRPQLHEVHRACC	235					
DB	214 -----QACC	217					
RESULT 7							
ID TR1A MOUSE STANDARD; PRT; 454 AA.							
AC	DT	01-MAY-1992 (Rel. 22, Created)					
DT	DT	01-MAY-1992 (Rel. 22, Last sequence update)					
DE	DT	15-SEP-2003 (Rel. 42, Last annotation update)					
DE	DT	Tumor necrosis factor receptor superfamily member 1A precursor (p60)					
DE	DT	(TNF-R1) (TNF-R1) (p95)					
DN	GN	TNFRSF1A OR TNFR1 OR TNFR-1.					
OS	OS	Mus musculus (Mouse)					
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	OX	NCBI_TaxID:10090;					
RP	RP	SEQUENCE FROM N.A.					
RP	RP	MEDLINE=91187885; PubMed=1849278;					
RA	RA	Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,					
RA	RA	Wong G.H., Chen E.Y., Goeddel D.V.;					
RT	RT	"Cloning and expression of cDNAs for two distinct murine tumor					
RT	RT	necrosis factor receptors demonstrate one receptor is species					
RT	RT	specific.";					
RL	RL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).					
RP	RP	SEQUENCE FROM N.A.					
RP	RP	MEDLINE=91246168; PubMed=1645445;					
RX	RX	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,					
RA	RA	Copeland N.G., Jenkins N.A., Smith C.A.;					
RT	RT	"Molecular cloning and expression of the type 1 and type 2 murine					
RT	RT	receptors for tumor necrosis factor.";					
RL	RL	Mol. Cell. Biol. 11:3020-3026 (1991).					
RP	RP	SEQUENCE FROM N.A.					
RP	RP	MEDLINE=91285014; PubMed=1647956;					
RA	RA	Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissenerghis A.M.,					
RA	RA	Gray P.W., Feldmann M., Foxwell B.M.J.;					
RT	RT	"Cloning, expression and cross-linking analysis of the murine p55					
RT	RT	tumor necrosis factor receptor.";					
RL	RL	Eur. J. Immunol. 21:1649-1656 (1991).					
RP	RP	SEQUENCE FROM N.A.					
RP	RP	TISSUE=Spleen;					
RC	RC	MEDLINE=92039815; PubMed=1657766;					
RX	RX	Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;					
RT	RT	"Molecular cloning and expression of the mouse Tnf receptor type b.";					
RT	RT	Immunogenetics 34:338-340 (1991).					
RL	RL	SEQUENCE FROM N.A.					
RP	RP	MEDLINE=94245292; PubMed=8188324;					
RP	RP	GO: 00007166; P: cell surface receptor linked signal transdu. . . IMP.					

DR GO; GO:0006952; P:defense response; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0007515; P:lymph gland development; IMP.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT  
 FT DOMAIN 22 212  
 FT TRANSMEM 213 235  
 FT DOMAIN 236 454  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 339 349  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT DISULFID 185 191  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 202 202  
 FT CONFLICT 394 394  
 SQ SEQUENCE 454 AA; 50129 MW; 0710C2B8C32B6D9 CRC64;

Query Match  
 Beat Local Similarity 7.0%; Score 157; DB 1; Length 454;  
 Matches 76; Conservative 21.0%; Pred. No. 0.00011;

34 CRQEFDRSRGNCVPCNQCGMELSKGCGYGEDAQCVTRLHRFKEDWGF-QKCKPC 92  
 44 CPQGYVHSHKNSICTCKHKGTVLVSDCP-SPGRDTCRECEKGTFTASQNYLRQCLSC 102  
 93 LDC-AVNNRFQKNCATSDAICG-----DCLPGFYRKTKL----- 127  
 103 KTCRKEMSVSEISPCQADKDTVCCKENQFQYLSETHFQCVDCSPCFNGVTVPCKETQ 162  
 128 -----VGF--QDMCEVCPGDPPEPHPCASKVNLVKIA-----STASSPRDTALA 173  
 163 NTVNCNCHAGFLRESECVPCS-----HCKNEECWKCLPPPLANVTNPQDSGTAVL 214  
 174 ICSALATVLLALLILCVYCKRQPMKPKNSLSQDIQYNGSELSCFDRPQLHEAHRA 233  
 215 L---PLVILLGLCLLSFIFI--SLMCRVPRW-----RPEVYSII--- 248  
 234 CCQCRDSV-----QTCG-PVRLPLSMCCCEACSNPATLGGVHSAASLQARN----- 281  
 249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSPSTGFPN-TLGFSTPGFSPSTPIPIFG 303  
 282 -----AGPAGEMVPTFGS--LTQISCG---EFSDAWPLMOMPMGDDNISFCDSYDEL 329  
 304 PSNWHFPPVSEVVTQDAPLLVSLCSVPAPTSVQKWDNSAHPQRPDNLAILYAVV 363  
 330 TG 331

Db 364 DG 365  
 RESULT 8  
 TR16\_CHICK  
 ID TR16\_CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)  
 DE (975 ICD) (Low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90166579; PubMed=2560385;  
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,  
 RA Shooter E.M., Reichardt L.F.;  
 RT "Structure and developmental expression of the nerve growth factor  
 RT receptor in the chicken central nervous system.";  
 RL Neuron 2:1123-1134 (1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE=90152140; PubMed=2154393;  
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;  
 RT "Structure and developmental expression of the chicken NGF receptor.";  
 RL Dev. Biol. 137:287-304 (1990).  
 CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,  
 CC and NT-4. Can mediate cell survival as well as cell death of  
 CC neural cells (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and  
 CC TRAF6 (By similarity). Type I membrane protein.  
 CC -!- PTM: N- AND O-glycosylated.  
 CC -!- PTM: Phosphorylated on serine residues.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 DR PIR; JN0006; JN0006.  
 DR HSP; P07174; INGR.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 DR Repeat; Phosphorylation; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 416  
 FT  
 FT DOMAIN 29 239  
 FT TRANSMEM 240 261  
 FT DOMAIN 262 416  
 FT REPEAT 23 57  
 FT REPEAT 58 99  
 FT REPEAT 100 138  
 FT REPEAT 140 180  
 FT DOMAIN 333 410  
 FT DOMAIN 188 236  
 FT DISULFID 24 35  
 FT DISULFID 36 49  
 FT DISULFID 39 56

FT DISULFID 59 75 BY SIMILARITY.  
 FT DISULFID 78 91 BY SIMILARITY.  
 FT DISULFID 81 99 BY SIMILARITY.  
 FT DISULFID 101 114 BY SIMILARITY.  
 FT DISULFID 117 130 BY SIMILARITY.  
 FT DISULFID 120 138 BY SIMILARITY.  
 FT DISULFID 141 156 BY SIMILARITY.  
 FT DISULFID 159 172 BY SIMILARITY.  
 FT DISULFID 162 180 BY SIMILARITY.  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 36 36 C -> Y (IN REF. 2).  
 FT CONFLICT 173 173 T -> K (IN REF. 2).  
 FT CONFLICT 276 276 N -> S (IN REF. 2).  
 FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 68CEAAB54F4D2D56 CRC64;

Query Match 6.6%; Score 148; DB 1; Length 416;  
 Best Local Similarity 31.0%; Pred. No. 0.00046;  
 Matches 58; Conservative 17; Mismatches 80; Indels 32; Gaps 11;

Qy 20 LGLYLSCKVTC-ESGD- - - - -CRQBFDR- -SGNCVPCNCGPMBELSKCEGFGY- - - - -G 67  
 Db 82 VGLHMSAPCVESDDAVCRCAVGYFQDELSSCKECSIC- - - - -EVGFLMPPCRDS 133  
 Qy 68 EDAQCVTCLRHFKEDWGFQKCKPLDCAVV- - -NRFOKANCATSDAICDCLPGFYRKT 125  
 Db 134 QDVTCEECPEGTFSDEANF- - -VDPCLPCTICEENEVMVKECTATSDAECRDLHPRWTH 191  
 Qy 126 -KLGFQDMCEVCGDEPPPPYEPHCASKVNLVKTASTASSP- - -RDYA- - -LAAVICSALA 179  
 Db 192 PSLAGSDSPE- - -PITRDPFNTGEMATTIADIVTTVMGSSQPVVSGRTADNLIPIVYCSILA 249  
 Qy 180 TVLLALL 186  
 Db 250 AVVGLV 256

RESULT 9  
 TNR3 HUMAN  
 ID TNR3 HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 3 precursor  
 DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
 DE protein) (Tumor necrosis factor C receptor).  
 GN LTR OR TNFRSF3 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human l2p  
 RT transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
 RA Butterch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710 (1994).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=99223511; PubMed=10207006;  
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell  
 RT death in HeLa cells.";  
 RL J. Biol. Chem. 274:11868-11873 (1999).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=20261554; PubMed=10799510;  
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,  
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
 RT "The lymphotoxin-beta receptor is necessary and sufficient for  
 RT LIGHT-mediated apoptosis of tumor cells.";  
 RL J. Biol. Chem. 275:14307-14315 (2000).  
 RN [6]  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=96278943; PubMed=8663299;  
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
 RA Yagita H., Okumura K.;  
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
 RT the lymphotoxin-beta receptor.";  
 RL J. Biol. Chem. 271:14661-14664 (1996).  
 RN [7]  
 RP INTERACTION WITH TRAF4.  
 RX PubMed=9626059;  
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,  
 RA Gascoyne R.D., Berner K., McFadden D., Shabalik A., Hugh J.,  
 RA Reynolds A., Cleveland C.V., Reed J.C.;  
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal  
 RT adult, fetal, and tumor tissues.";  
 RL Am. J. Pathol. 152:1549-1561 (1998).  
 RN [8]  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=98172745; PubMed=9511754;  
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.-I.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140 (1998).  
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
 CC and TRAF5. May play a role in the development of lymphoid organs.  
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 CC -----

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DR EMBL; L04270; AAA36757.1; -.
DR EMBL; BC026262; AAH26262.1; -.
DR PIR; I54182; I54182.
DR HSSP; P25942; 1CDF.
DR Genew; HGNC:6718; TNFR.
DR MIM; 600979; -.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_C6; 4.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 6.5%; Score 146.5; DB 1; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.0063;
Matches 73; Conservative 42; Mismatches 107; Indels 119; Gaps 19;

Qy 16 LVLVGLYLCK-----VTCSGDCRQOE---FRDRSGMVCPCNQCPCGMELSKECGFG 65
Db 18 VLGLFGLLAASQAPVPPYASQNTCRDQEKVEYEPQHRIC--CSRCPPTGYVSACK--S 73

Qy 66 YGEDAQCVTCRLHRFKEDWGF-----QKCKPC-----LDCAVNRFOKANCATSDAIC- 114
Db 74 RIRDTVCATCAENSYNEHWNLYLTICLCRCPDVMGLEETAPCTSKRKTQCRCQPGMFCA 133

Qy 115 -----GDLCPGFYRKTK-LVGFQDMECVPC-----GPPPPYPBPH--CAS 151
Db 134 AWALECTHCELLSDCPGTETAELEKDEVGKGNHCVPCKAGHFQNTSSPASCQPHTCEN 193

Qy 152 KVNILVKIA-----STASSPRD-----TALAAVICSALATVLLALLILCVIY---- 192
Db 194 Q-GLVEAAGPTAQSDTTCKNPLEPLPPEMSGTLMMLAVLLPLAPFLLLATVFCIWKSH 252

Qy 193 --CKR--QFMEKXP-----SWSLRSDIQYNGSELSCEPRPQIHEYAHACQCR 238
Db 253 SLCKKGLSLKRRPQSGPNPVAGSW-----SGDVSPVSTGLPAAPVLEA 316

Qy 239 RDSVQTCGPVRLLPSCMECEACSPNPATLGCVHSAASLOA 279
Db 288 PDLVQPLLPI-----SGDVSPVSTGLPAAPVLEA 316

RESULT 10
TNR4 RAT
ID TNR4 RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE TNFRSF4 OR TXGPIL OR OX40.
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBO J. 9:1063-1068(1990).
CC -1- FUNCTION: Receptor for TNFRSF4/OX40L/GP34.
CC -1- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; X17037; CA434897.1; -.
DR PIR; S12783; S12783.
DR HSSP; O14763; 1D4V.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 20 210
FT TRANSMEM 211 235
FT DOMAIN 236 271
FT REPEAT 25 60
FT REPEAT 61 102
FT REPEAT 103 123
FT REPEAT 124 164
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 76
FT DISULFID 79 94
FT DISULFID 82 102
FT DISULFID 104 122
FT DISULFID 125 138
FT DISULFID 144 163
FT CARBOHYD 143 143
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 6.4%; Score 145; DB 1; Length 271;
Best Local Similarity 29.8%; Pred. No. 0.00047;
Matches 57; Conservative 19; Mismatches 75; Indels 40; Gaps 13;

Qy 9 QEKTFTLLVL-LGY----LSC-KVTCSGDCRQOEFRDRSGMVCPCNQCPCGMELSKECG 63
Db 6 QQPTAFLLGLSLGVTVKLNCVXDTPYPSGH-----KC--CRECQPGHGWSR- 51

Qy 64 FGVEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVNRFO--KANCATSDAICGDLCPGFY 122
Db 52 -DHTRTVCHPCPGPGFYNEAVNTDCKQTCQNHRSSELKQNTPTDITVC-QCRPGTQ 109

Qy 123 RKTGLVGFQDMECVPCGDPPTPPYEP-----HCASKVNLV-----KIASTASSPRDTALAAVI 174

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Db 110 PRODSHKLGVDCVPC--PPGHFSPGNSQACKPMTNCTLSGKQIRHPASNSLDT-----V 162
Qy 175 C---SALATVL 182
Db 163 CEDRSLLATLL 173

RESULT 11
TNR4 MOUSE
ID TNR4 MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
GN TNRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Feli H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions.";
RL J. Immunol. 151:5261-5271 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein.";
RL Eur. J. Immunol. 25:926-930 (1995).
CC -1- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
CC -1- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; Z21674; CAA79772.1; -.
DR EMBL; X85214; CAA59476.1; -.
DR PIR; I48700; I48700.
DR HSP; O14763; 1D0G.
DR MGD; MGI:104512; Tnfrsf4.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0006988; P:cellular defense response; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 20 272
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 4.
FT DOMAIN 20 211
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236
FT DOMAIN 237 272
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 26 61
FT TNR-CYS 1.
FT REPEAT 62 103
FT TNR-CYS 2.

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FT REPEAT 104 124
FT REPEAT 125 165
FT DISULFID 27 38
FT DISULFID 39 52
FT DISULFID 42 60
FT DISULFID 63 77
FT DISULFID 80 95
FT DISULFID 83 103
FT DISULFID 105 123
FT DISULFID 126 139
FT DISULFID 145 164
FT CARBOHYD 144 144
FT CONFLICT 15 15
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 6.4%; Score 144; DB 1; Length 272;
Best Local Similarity 29.5%; Pred. No. 0.00056;
Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;

Qy 15 TLIVLLGLYSCKVTCSGDCRQEFDRDSGN-CVPCNQCGPMELSKCEGFGYGEDAQCV 73
Db 9 TALLLLA-LTLGVYARLNCVKHTY--PSGHKC--CRECQPGHGMVSRG--DHTFDTLCH 61
Qy 74 TCRHREFKEDWGFQKCKPCLDCAVVRFPQ-KANCSATSDAICGDCLPFGYVKTKLVGFQD 132
Db 62 PCETGFYNEAVNYDTCQCTQCNHRSGSELKQNCPTQDTVC-RCRPGTQPR-----QD 114
Qy 133 -----MECVPCGDPDPYPSP-----HCASKVNLVKIATASSPRDTALAIVC---SALA 179
Db 115 SGYKLGVDVCPC--PPGHFSPGNNQACKPMTNCTLSGKQIRHPASDSLDV-CEDRSLLA 171
Qy 180 TVL 182
Db 172 TLL 174

RESULT 12
LMB2 RAT
ID LMB2 RAT STANDARD; PRT; 1801 AA.
AC P15800;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).
GN LAMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89159410; PubMed=2922051;
RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;
RT "A laminin-like adhesive protein concentrated in the synaptic cleft
RT of the neuromuscular junction.";
RL Nature 338:229-234 (1989).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT

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WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

-!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.

-!- SIMILARITY: Contains 1 laminin N-terminal domain.

-!- SIMILARITY: Contains 13 laminin EGF-like domains.

-!- SIMILARITY: Contains 1 laminin IV domain.

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EMBL; X16563; CAA34561.1; ..

PIR; S03539; MMRPTS.

HSSP; P02468; 1KLO.

InterPro; IPR006209; EGF like.

InterPro; IPR002049; Laminin\_EGF.

InterPro; IPR001886; LamNT.

Pfam; PF00053; laminin\_EGF\_13.

Pfam; PF00055; laminin\_Nterm; 1.

PRINTS; PR00011; EGF\_LAMININ.

SMART; SM00180; EGF\_Lam; 13.

SMART; SM00136; LamNT; 1.

PROSITE; PS00022; EGF\_1; 10.

PROSITE; PS01186; EGF\_2; 2.

PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.

Glycoprotein; Basal membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

SIGNAL 1 35

CHAIN 36 1801 LAMININ BETA-2 CHAIN.

DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).

DOMAIN 286 349 LAMININ EGF-LIKE 1.

DOMAIN 350 412 LAMININ EGF-LIKE 2.

DOMAIN 413 472 LAMININ EGF-LIKE 3.

DOMAIN 473 524 LAMININ EGF-LIKE 4.

DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).

DOMAIN 556 785 LAMININ DOMAIN IV.

DOMAIN 786 833 LAMININ EGF-LIKE 6.

DOMAIN 834 879 LAMININ EGF-LIKE 7.

DOMAIN 880 929 LAMININ EGF-LIKE 8.

DOMAIN 930 988 LAMININ EGF-LIKE 9.

DOMAIN 989 1040 LAMININ EGF-LIKE 10.

DOMAIN 1041 1097 LAMININ EGF-LIKE 11.

DOMAIN 1145 1192 LAMININ EGF-LIKE 12.

DOMAIN 1146 1192 LAMININ EGF-LIKE 13.

DOMAIN 1193 1412 DOMAIN II.

DOMAIN 1413 1445 DOMAIN ALPHA.

DOMAIN 1446 1801 DOMAIN I.

DOMAIN 1259 1306 COILED COIL (POTENTIAL).

DOMAIN 1475 1529 COILED COIL (POTENTIAL).

DOMAIN 1576 1793 COILED COIL (POTENTIAL).

DISULFID 286 295 BY SIMILARITY.

DISULFID 288 313 BY SIMILARITY.

DISULFID 315 324 BY SIMILARITY.

DISULFID 327 347 BY SIMILARITY.

DISULFID 350 359 BY SIMILARITY.

DISULFID 352 377 BY SIMILARITY.

DISULFID 380 389 BY SIMILARITY.

DISULFID 392 410 BY SIMILARITY.

DISULFID 413 426 BY SIMILARITY.

DISULFID 415 441 BY SIMILARITY.

DISULFID 443 452 BY SIMILARITY.

DISULFID 455 470 BY SIMILARITY.

DISULFID 473 487 BY SIMILARITY.

DISULFID 475 494 BY SIMILARITY.

DISULFID 496 505 BY SIMILARITY.

DISULFID 508 522 BY SIMILARITY.

DISULFID 786 798 BY SIMILARITY.

DISULFID 788 805 BY SIMILARITY.

DISULFID 807 816 BY SIMILARITY.

DISULFID 819 831 BY SIMILARITY.

FT	DISULFID	834	846	BY SIMILARITY.
FT	DISULFID	836	853	BY SIMILARITY.
FT	DISULFID	855	864	BY SIMILARITY.
FT	DISULFID	867	877	BY SIMILARITY.
FT	DISULFID	880	889	BY SIMILARITY.
FT	DISULFID	882	896	BY SIMILARITY.
FT	DISULFID	899	908	BY SIMILARITY.
FT	DISULFID	911	927	BY SIMILARITY.
FT	DISULFID	930	946	BY SIMILARITY.
FT	DISULFID	932	957	BY SIMILARITY.
FT	DISULFID	959	968	BY SIMILARITY.
FT	DISULFID	971	986	BY SIMILARITY.
FT	DISULFID	989	1003	BY SIMILARITY.
FT	DISULFID	991	1010	BY SIMILARITY.
FT	DISULFID	1013	1022	BY SIMILARITY.
FT	DISULFID	1025	1038	BY SIMILARITY.
FT	DISULFID	1098	1110	BY SIMILARITY.
FT	DISULFID	1100	1117	BY SIMILARITY.
FT	DISULFID	1119	1128	BY SIMILARITY.
FT	DISULFID	1131	1143	BY SIMILARITY.
FT	DISULFID	1146	1158	BY SIMILARITY.
FT	DISULFID	1148	1165	BY SIMILARITY.
FT	DISULFID	1167	1176	BY SIMILARITY.
FT	DISULFID	1179	1190	BY SIMILARITY.
FT	DISULFID	1193	1193	INTERCHAIN (PROBABLE).
FT	DISULFID	1196	1196	INTERCHAIN (PROBABLE).
FT	DISULFID	1800	1800	INTERCHAIN (PROBABLE).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	371	371	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1252	1252	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1311	1311	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1351	1351	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1502	1502	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1801 AA;	196473 MW;	97AEF32F8F3FA75 CRC64;

Query Match 6.3%; Score 142.5; DB 1; Length 1801;

Best Local Similarity 22.6%; Pred. No. 0.0067;

Matches 98; Conservative 33; Mismatches 147; Indels 155; Gaps 27;

Qy	17	LVLGLYLSCKVTCSGDCRQCFRDRSGNVCNQCQGNHLSKEC-----GFG--- 65
Db	778	LVTNGALPCQ--CDPQGLSSECNPHGGQC---RCKPGV-VGRRCDACATGYGFGPAG 830
Qy	66	-----VGEDAQCVCRLHRF-----KEDMGFOCKPCDCAVVRNF 101
Db	831	CQACQCPDGLSALCEGTSGQCL-CETGAFGLRCDHCQGWGFPNCRFC-----VNG 884
Qy	102	QKANCATSDAI-----CGDCLPGFYRKTCL-VGFQDMCVPCGDPP-PPYEPH 148
Db	885	RADECDATGACLCGRDYGEGHCEHCERCIAGHGDPRLPYGGQ---CRPCPCPEGSGQRH 941
Qy	149	CASKNVLKTIASPRDTALAATVLLALLILCVYCKQFME-KKPSWLR 207
Db	942	FAT-----SCHRDGYSQOIVCHCRAGY---TGLRCEACAPGHGDPSPGRCQ 987
Qy	208	-----SODIQ-----YNGSELSGCFD-----RPLHEYA-----HRACCCRR 239
Db	988	LCSCSGNIDTPDGACDPHTGQCRLHHTGPHGCHGCKFGHQAARQSRCTCNLLG 1047
Qy	240	DSVQTC-----GPVRLLP---SMCCBEACSPN---PATLGGVHSAASLQARNA 282
Db	1048	TDQRCPSTDLCHCDPSTGCPCLPHVQGLSCDR-CAPNFWNFTSGRCQPCACHPSRAR 1106
Qy	283	GP-----AGEWVTFPGSLTQSCGFSDAWPLMQ-----NPMGGD----- 318
Db	1107	GPTCNEFTGCHCHAG-----EGGRTSCSQSLHMGDPGLQCRACDPRGDKPOCHR 1160
Qy	319	NISFCDSYBELTG 331
Db	1161	STGHCSRCRFGVG 1173

RESULT 13  
 ID\_NFX1\_HUMAN STANDARD; PRT; 1104 AA.  
 AC Q12986;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Transcriptional repressor NF-X1 (EC 6.3.2.-) (Nuclear transcription factor, X box-binding, 1).  
 GN NFX1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=95053707; PubMed=7964459;  
 RA Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;  
 RT "A novel cysteine-rich sequence-specific DNA-binding protein interacts with the conserved X-box motif of the human major histocompatibility complex class II genes via a repeated Cys-His domain and functions as a transcriptional repressor.";  
 RT J. Exp. Med. 180:1763-1774(1994).  
 RL [2]  
 FN FUNCTION AS A E2-DEPENDENT UBIQUITIN LIGASE.  
 RP MEDLINE=99432238; PubMed=10500182;  
 RA Lorick K.L., Jensen J.P., Fang S., Ong A.M., Hatakeyama S., Weissman A.M.;  
 RT "RING fingers mediate ubiquitin-conjugating enzyme (E2)-dependent ubiquitination.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 96:11364-11369(1999).  
 RL [3]  
 FN FUNCTION: Repressor of HLA-DRA transcription. Binds to the X-box motif of MHC class II genes. May play an important role in regulating the duration of an inflammatory response by limiting the period in which MHC class II molecules are induced by interferon-gamma. Mediates E2-dependent ubiquitination.  
 CC [4]  
 FN SUBCELLULAR LOCATION: Nuclear.  
 CC [5]  
 FN INDUCTION: By interferon gamma.  
 CC [6]  
 FN DOMAIN: The RING-type zinc finger domain interacts with an ubiquitin-conjugating enzyme (E2) and facilitates ubiquitination.  
 CC [7]  
 FN SIMILARITY: Contains 1 RING-type zinc finger.  
 CC [8]  
 FN SIMILARITY: Contains 1 R3H domain.  
 CC [9]  
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 CC [10]  
 EMBL: U15306; AAA69517.1; -;  
 DR EPR; I38869; I38869.  
 DR TRANSFAC; T01694; -;  
 DR GENBANK; HGNC:7803; NFX1.  
 DR MIM; 603255; -;  
 DR GO; GO:0003700; F:transcription factor activity; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0001222; P:negative regulation of transcription from P. . .; TAS.  
 DR GO; GO:0006366; P:transcription from Pol II promoter; TAS.  
 DR InterPro; IPR001374; R3H.  
 DR InterPro; IPR000967; Znf\_NFX1.  
 DR InterPro; IPR001965; Znf\_PHD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF01424; R3H; 1.  
 DR Pfam; PF00097; Zf-C3HC4; 1.  
 DR Pfam; PF01422; Zf-NFX1; 8.  
 DR SMART; SM00393; R3H; 1.  
 DR SMART; SM00184; RING; 1.  
 DR SMART; SM00438; Znf\_NFX1; 9.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 KW Ub1 conjugation pathway; Ligase; Transcription regulation; Repressor;

DNA-binding; Nuclear protein; Repeat; Zinc-finger.  
 ZN FING 342 393 RING-TYPE  
 FT DOMAIN 424 876 7 X APPROXIMATE REPEATS, CYS-RICH.  
 FT REPEAT 424 463 1.  
 FT REPEAT 480 517 2.  
 FT REPEAT 541 580 3.  
 FT REPEAT 606 647 4.  
 FT REPEAT 695 734 5.  
 FT REPEAT 806 842 6.  
 FT REPEAT 843 876 7.  
 FT DOMAIN 992 1041 R3H.  
 FT DOMAIN 1068 1073 POLY-PRO.  
 SQ SEQUENCE 1104 AA; 123149 MW; 36FEC4292F78130C CRC64;  
 Query Match 6.3%; Score 142; DB 1; Length 1104;  
 Best Local Similarity 18.8%; Pred. No. 0.0041;  
 Matches 110; Conservative 58; Mismatches 182; Indels 236; Gaps 27;  
 QY 24 SKVTCESGDCROEFRDRSGNVCNQCQPGMELSKGCG-----FGYGEDAQ----- 72  
 DB 440 SCNLLCHPG-----PCPPCPAFMTKTCCEGRTRHTVRCGQAVSVHCNSNPC 484  
 QY 73 ---VTCRLHPRKEDWGFQKPCLDCAVNRFOKANCATS-DAICGDCLPGFVRKTLV 128  
 DB 485 ENILNCQHQAELCHGGQCPCQ--IILN--QVCYCGSTRDVLCTGV-----GKSD 534  
 QY 129 GFODMEC-----VPCGD-----PPP-----PYEPHC--ASKNVLVKIATASS 164  
 DB 535 GFDFSCCLKTCGDKLKGNTCSQVCHPQCQCQCPRLPQLVRCPCQQTFLSLLGLSS 594  
 QY 165 PRDTALAAV-----IC-SALATVLLALLILC-----VIYCKQFMKK- 201  
 DB 595 SRKTCMDPVSCGKVGKPLPCGSLDFIHTCEKLCHEGDCGVPVSRTSVISCRCSTFKEL 654  
 QY 202 PSWSLSQDI-----QNGSELSCFDRPQ-----LH---EYA 230  
 DB 655 PCTSLKSEDATFMCDCRCKNKKRLCGRHKCNIEICVDKHKCPLNCGRKLRCGLHRCBEP 714  
 QY 231 HRACCO-CRRDSVQT---CGPVRLLLPSMCC-----EE 258  
 DB 715 HRGNCQTCWQSFDELTCGASVIPPVPCGTRPPECTQTCARVHECDHPVHSHSEE 774  
 QY 259 ACS-----PNPATLGCGVHSAASL----- 277  
 DB 775 KCPCTFLTQKCMGKHEPRSNIPCHLVDSICGLPCSATLPCGMHKKQRLCHKGECCLVDE 834  
 QY 278 -----QAR-----NAGPAGEMVTFFGSLTQSI 300  
 DB 835 PKQPCTTPRADCGHPCMAPCHTSSPCPVTAACKAVELQCECGRRKEMVICSEASSTYQR 894  
 QY 301 CGEFSDAWPLMQNPMGNDNISFCDSYPELTGEDIHSLNPELSSTLSNSSLQDLVGAV 360  
 DB 895 IAIISMASKITDMQLGGS-----VEISKLTKEVHQARLEDECSALEKKR--LAEP 948  
 QY 361 PVQSHENFTAAATDLGRYNNLTVESASTQDALTMRSQDQSGAI 406  
 DB 949 HISEDSPFNIRSSGSKFSDSLAKEDA--RKDLKFVSDVEKEMETLV 992  
 RESULT 14  
 ID\_TRIA\_RAT STANDARD; PRT; 461 AA.  
 AC P22934; Q91V30; Q91Y93;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p50)  
 DE (TNF-R1) (TNF-RI) (p55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

[1]  
 SEQUENCE FROM N.A.  
 MEDLINE=91090841; PubMed=1702293;  
 Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 Lantz M., Olson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 "Molecular cloning and expression of human and rat tumor necrosis  
 factor receptor chain (p60) and its soluble derivative, tumor  
 necrosis factor-binding protein.";  
 DNA Cell Biol. 9:705-715(1990).  
 [2]  
 SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.  
 STRAIN=BB(DR)/Wot, LEW/NHsd, ACI/SegHsd, DA/Bkl, F344/NHsd, and  
 BN/SeHsd;  
 Furuya T., Salstrom J.L., Bina J., Hashimoto A., Dobbins D.E.,  
 Wilder R.L., Remmers E.F.;  
 "Polymorphisms of the tumor necrosis factor receptor type 1 locus  
 among autoimmune susceptible and resistant inbred rat strains.";  
 Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 -!- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric  
 TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 caspase-8 to the activated receptor. The resulting death-inducing  
 signaling complex (DISC) performs caspase-8 proteolytic activation  
 which initiates the subsequent cascade of caspases (aspartate-  
 specific cysteine proteases) mediating apoptosis (By similarity).  
 -!- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 homotrimerization. The aggregated death domains provide a novel  
 molecular interface that interacts specifically with the death  
 domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 RIP and possibly FADD, are recruited to the complex by their  
 association with TRADD. This complex activates at least two  
 distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 Binds BAQ4 (By similarity).  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 -!- SIMILARITY: Contains 1 death domain.  
 -----  
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 -----  
 EMBL; M63122; AAA42256.1; -;  
 EMBL; AF329976; AAK53562.1; -;  
 EMBL; AF329977; AAK53563.1; -;  
 EMBL; AF329981; AAK53567.1; -;  
 EMBL; AF329978; AAK53564.1; -;  
 EMBL; AF329979; AAK53565.1; -;  
 EMBL; AF329980; AAK53566.1; -;  
 PIR; B36555; GQRTT1.  
 HSSP; P19438; INCF.  
 InterPro; IPR000488; Death.  
 InterPro; IPR01368; TNFR\_c6.  
 Pfam; PF00531; Death; 1.  
 Pfam; PF00020; TNFR\_c6; 4.  
 SMART; SM00005; DEATH; 1.  
 SMART; SM00208; TNFR; 4.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 SIGNAL 1 21  
 CHAIN 22 461  
 DOMAIN 22 211  
 TRANSMEM 212 234  
 DOMAIN 235 461  
 REPEAT 43 82  
 TNFR-CYS 1.  
 TNFR-CYS 2.  
 TNFR-CYS 3.  
 TNFR-CYS 4.

FT DOMAIN 344 354 N-SWASE ACTIVATION DOMAIN (NSD).  
 FT 363 448 DEATH.  
 FT DISULFID 44 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 81 BY SIMILARITY.  
 FT DISULFID 84 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 195 BY SIMILARITY.  
 FT DISULFID 185 191 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARIANT 230 230 I -> V (IN STRAINS LEW/NHSD, ACI/SEGHS,  
 DA/BKL AND F344/NHSD).  
 FT VARIANT 295 295 H -> P (IN STRAINS LEW/NHSD, ACI/SEGHS,  
 DA/BKL, F344/NHSD AND BN/SSNHSD).  
 SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FED202 CRC64;  
 Query Match 6.3%; Score 141.5; DB 1; Length 461;  
 Best Local Similarity 21.6%; Pred. No. 0.0016;  
 Matches 72; Conservative 37; Mismatches 113; Indels 111; Gaps 20;  
 QY 34 CRQEFRRSGNVCNQCQPGMELSKGCGYGVGDAQCVCVTLRHRPKEDWGQKPKCL 93  
 DB 44 CPQGYAHPKNNIGICCTCKHGYLVSDCP-SPQGTVCVEVCKDGTFTASQ--NHVRQCL 100  
 QY 94 DCAVNR--POK--ANCSATSDAICDCLPFGFYRTKLVGFQDMECVPC----- 138  
 DB 101 SCTCRKEMFQVEISPKAMDVTVCCKKQKQRYLSETHFQCVDGSCPCFNVTTPCKE 160  
 QY 139 -----GDPPPPYEPHCASKVNLVKI-----ASTASSPRDTALAAVICSALA 179  
 DB 161 KQNTVCNCHAGFFLSNGECTPCS-HCKKNQECMKCLPPVANVTNPQDSGTAVLLPLVIF 219  
 QY 180 TVLLALLILCV-IVCKRQPMKPSLSRLSDIYNGSELSCFDPOLHVEYHRAACQCR 238  
 DB 220 LGCLCLFFICISLLC-----RYPQW-----RPRVYSII-----C- 248  
 QY 239 RDSVQTCGVR-----LLPSMCCCEACSNPA---TLGCGV-----HSAASLQA 279  
 DB 249 RDS-----APVEVEGEGIVTKPLTPASI--PASPMPGPNFTLQSTTPRFSHPVSSTPI 302  
 QY 280 RNA-GPAG-----EMVPT-----FFGSL 296  
 DB 303 SPVFGFSNMHNFVPPVREVPTQGDPLLYGSL 335  
 RESULT 15  
 TRLT MACFA  
 ID TRLT MACFA STANDARD; PRT; 430 AA.  
 AC QSN092;  
 DT 28-FEB-2003 (Rel. 41, Created).  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 19L precursor  
 DE (Receptor expressed in lymphoid tissues).  
 GN TNFRSF19L OR RELT.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21458551; PubMed=11574149;  
 RA Osada N., Hida M., Kueuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,  
 Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kueusda J.;

RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human  
RL chromosomes";  
CC -!- FUNCTION: Mediates activation of NF-kappa-B (By similarity). May  
CC play a role in T-cell activation.  
CC -!- SUBUNIT: Associates with TRAF1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
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CC -----  
DR EMBL; AB046039; BAB01621.1; -;  
DR InterPro; IPR001368; TNFR\_C6.  
DR SMART; SMO0208; TNFR; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 430  
FT DOMAIN 27 162  
FT TRANSMEM 163 183  
FT DOMAIN 184 430  
FT REPEAT 50 90  
FT DISULFID 51 65  
FT DISULFID 71 90  
FT CARBOHYD 149 149  
FT SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;  
SQ  
  
Query Match 6.2%; Score 141; DB 1; Length 430;  
Best Local Similarity 25.6%; Pred. No. 0.0016;  
Matches 44; Conservative 23; Mismatches 57; Indels 48; Gaps 6;  
  
Qy 51 QCGPGMELSKCGFGYGEDACVTCRLHREKEDMGFKPCCLDCAVVNRQKANCST 110  
Db 31 QCPPG-----EFDLPNGGTLRCPCPGPTGTFSAAMGSSPCQPHARCSLQRRLAEQVGTATQ 86  
Qy 111 DAICGDCCLPGFYRKTCLVGFQDMECVPCGDPDPVPEPHCASKVNL-----VK 157  
Db 87 DTLGDCWPGWFG-----PWGVRVPCQPCSWAPLGIHGCDWGRARRGVE 133  
Qy 158 IASTASS-----PRDTALA-AVICSALATVLLALLILCVIYC 193  
Db 134 VAAGASSGGTTRQPGNGTRAGGPETAAQYAVI--AIVPVFLMGLLLILVC 183

Search completed: January 29, 2004, 21:39:07  
Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 29, 2004, 21:36:16 ; Search time 40 Seconds  
(without alignments)  
2690.198 Million cell updates/sec

Title: US-09-780-532A-2

Perfect score: 2256

Sequence: 1 MALKVLEQETFTLLVLL.....LDQSGAIHPATQTSIQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1559.5	69.1	416 11 Q8BUM7	Q8Bum7 mus musculus
2	846.5	37.5	273 11 Q8BMR1	Q8Bmr1 mus musculus
3	497	22.0	297 11 Q8BX35	Q8Bx35 mus musculus
4	496	22.0	297 11 Q8BM50	Q8Bm50 mus musculus
5	488	21.6	318 4 Q8IZA6	Q8iza6 homo sapien
6	486	21.5	185 11 Q8BJ56	Q8bj56 mus musculus
7	172	7.6	387 13 Q9PVD4	Q9pvd4 xenopus lae
8	155	6.9	276 13 Q9DD02	Q9dd02 gallus gall
9	145	6.4	1024 4 Q9BX11	Q9bx11 homo sapien
10	142	6.3	1120 4 Q96EL5	Q96el5 homo sapien
11	141	6.2	436 11 Q8BT00	Q8btv0 mus musculus
12	140.5	6.2	548 5 Q9GQ45	Q9gq45 giardia lam
13	139	6.2	317 13 Q8JFV6	Q8jfv6 brachydanio
14	138.5	6.1	186 12 Q72735	Q72735 cowpox viru
15	136.5	6.1	350 12 Q57123	Q57123 cowpox viru
16	136	6.0	401 13 Q9PRG7	Q9prg7 xenopus lae

17	136	6.0	417	11	Q8BYY1	Q8byy1 mus musculu
18	136	6.0	427	11	Q8CFT3	Q8cft3 mus musculu
19	135.5	6.0	2813	11	Q8CIZ8	Q8ciz8 mus musculu
20	135	6.0	186	12	Q9YP87	Q9yp87 cowpox viru
21	135	6.0	348	12	O57108	O57108 monkeypox v
22	135	6.0	348	12	O57277	O57277 monkeypox v
23	135	6.0	348	12	O57103	O57103 monkeypox v
24	134	5.9	436	11	Q8BX43	Q8bx43 mus musculu
25	133.5	5.9	3396	5	Q9VM55	Q9vm55 drosophila
26	133	5.9	1650	11	Q9QVT6	Q9qvt6 rattus sp.
27	132.5	5.9	349	12	O57100	O57100 monkeypox v
28	132.5	5.9	349	12	O57101	O57101 monkeypox v
29	132.5	5.9	349	12	O57102	O57102 monkeypox v
30	132.5	5.9	349	12	O57099	O57099 monkeypox v
31	132.5	5.9	349	12	O57291	O57291 monkeypox v
32	132	5.9	235	13	Q8JFU6	Q8jfu6 brachydanio
33	131	5.8	186	12	Q9WJB4	Q9wjb4 vaccinia vi
34	131	5.8	347	12	O57115	O57115 cowpox viru
35	131	5.8	355	12	O85308	O85308 cowpox viru
36	130.5	5.8	1171	11	Q8CGB2	Q8cgb2 mus musculu
37	130.5	5.8	1799	11	Q8ROY0	Q8roy0 mus musculu
38	130	5.8	1827	13	Q8JHV6	Q8jhv6 brachydanio
39	129	5.7	186	12	Q911R5	Q911r5 vaccinia vi
40	129	5.7	349	12	O57305	O57305 cowpox viru
41	129	5.7	848	11	Q8C720	Q8c720 mus musculu
42	129	5.7	1792	13	O57484	O57484 gallus gall
43	129	5.7	3567	11	Q9ES77	Q9es77 mus musculu
44	128.5	5.7	349	12	O57111	O57111 variola vir
45	128	5.7	507	5	Q8MS81	Q8ms81 drosophila

## ALIGNMENTS

### RESULT 1

Q8BUM7	ID	Q8BUM7	PRELIMINARY;	PRT;	416 AA.
AC	Q8BUM7;				
DT	01-MAR-2003 (Tremblrel. 23, Created)				
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)				
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 19.				
OS	Mus musculus (Mouse)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Hippocampus;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium.				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."				
RL	Nature 420:563-573(2002).				
DR	EMBL; AK083283; BAC38842.1; .				
SQ	SEQUENCE 416 AA; 45256 MW; ODE295B591FA570A CRC64;				

Query Match	69.1%;	Score 1559.5;	DB 11;	Length 416;
Best Local Similarity	70.2%;	Pred. No. 8.6e-137;		
Matches 294;	Conservative 36;	Mismatches 84;	Indels 5;	Gaps 3;
Qy	1	MALKVLEQETFTLLVLLGYSCKVTCSSGDCRQQRQEFDRSGNCVPCNOCGPGMELSK	60	
			:::	
Db	1	MALKVLPFHRTVLPAAFLFLHLACKVSCSTGDCRQQRQEFDRSGNCVLCQCGPGMELSK	60	
			:::	
Qy	61	ECGFGYGEDAQCVTCRLHFRKEDWGFOCKPCLDCAVVRFPKANCATSDAICGDCCLPG	120	
			:::	
Db	61	ECGFGYGEDAQCVPCRPQRFKEDWGFOCKPCADCALVNRFPKANCSTHTSDAVCGDCCLPG	120	
			:::	
Qy	121	FYRKTKLVGFQDMECVPCGDPDPYPPHCKASKNLVKIASTASSPRDTALAAVTCALAT	180	
			:::	
Db	121	FYRKTKLVGFQDMECVPCGDPDPYPPHCKTSKNLVKISSTVSSPRDTALAAVTCALAT	180	
			:::	

```
QY 181 VLLALLILCVYCKRQFMEKPKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKRQFMEKPKPSWLSRSDIQYNGSELSCFDRPOLHEYAHRACCCRRD 240
QY 241 SVQTCGVRLLPSCCEACSPNATIGCGVHSAASLQARNAGPAGEMVPTFFGSLPQSI 300
DB 241 SAPMYGPHLLPSCCEARSSARAVLGCGLRSPPTLQERNPASVGDTPAFFGVSRSI 300
QY 301 CGEESDAPLPMONPMGGDNTSFCDSYBELTGEDTHSLNPELESSTLDSNSSQDLVCGAV 360
DB 301 CAEESDAPLPMONPMGGDNTSFCDSYBELTGEDTHSLNPELESSTLDSNSSQDLVCGAV 360
QY 361 PVQSHENFTAAATPLSRVNN--TLVESASTODALTMTESOLDQESGAIHHPATQTSLOEA 417
DB 359 -ALESSGNVSESTSPRHGDTGTWVEQTQAQDAQRTFSQGGWEDRENILAMPTAFQDA 416

RESULT 2
Q8BWR1 ID Q8BWR1 PRELIMINARY; PRT; 273 AA.
AC Q8BWR1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050282; BAC34152.1; -.
SQ SEQUENCE 273 AA; 29256 MW; B6A8E2E1F36B1769 CRC64;

Query Match 37.5%; Score 846.5; DB 11; Length 273;
Best Local Similarity 64.3%; Pred. No. 1.4e-70;
Matches 173; Conservative 26; Mismatches 65; Indels 5; Gaps 3;

QY 151 SKNVLVIKSTVSPRDTALAAVTCALATVLLALLILCVYCKRQFMEKPKPSWLSRSD 210
DB 8 SKNVLVIKSTVSPRDTALAAVTCALATVLLALLILCVYCKRQFMEKPKPSWLSRSD 67
QY 211 IOYNGSELSCFDRPOLHEYAHRACCCRRDSVQTCGVRLLPSCCEACSPNATIGCG 270
DB 68 IOYNGSELSCFDRPOLHEYAHRACCCRRDSVQTCGVRLLPSCCEACSPNATIGCG 127
QY 271 VHSAAISLQARNAGPAGEMVPTFFGSLTQSCGEPDAPLPMONPMGGDNTSFCDSYBELT 330
DB 128 LRSPTTLQERNPASVGDTPAFFGVSRSICAEESDAPLPMONPMGGDNTSFCDSYBELT 186
QY 331 GEDTHSLNPELESSTLDSNSSQDLVCGAVPVQSHENFTAAATPLSRVNN--TLVESAST 388
DB 187 GEDTHSLNPELESSTLDSNSSQDLVCGAVPVQSHENFTAAATPLSRVNN--TLVESAST 244
QY 389 QDALMTESOLDQESGAIHHPATQTSLOEA 417
DB 245 QDALMTESOLDQESGAIHHPATQTSLOEA 273

RESULT 3
Q8BX35 ID Q8BX35 PRELIMINARY; PRT; 297 AA.
AC Q8BX35
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
```

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to X-linked ectodysplasin-A receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK049134; BAC33562.1; -.
SQ SEQUENCE 297 AA; 33066 MW; 46F8FDDC51D739BE CRC64;

Query Match 22.0%; Score 497; DB 11; Length 297;
Best Local Similarity 40.2%; Pred. No. 5.6e-38;
Matches 97; Conservative 30; Mismatches 74; Indels 40; Gaps 3;

QY 33 DCQQQBFDRSRGNCVPCNCGPMELSKCEGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
DB 2 DCQENEYRDQWGRCVTCQQCGPQOELSKDCGYGEGDAHCIVCPPRKYKSTWGHRCQTC 61
QY 93 LDCAVNVRQKANCSDATSDAICGDCLPGRVYRKTGLVGFQDMCVPCGDPPPPPEHCASK 152
DB 62 ITCAVINRVQKANCNTNTSNAICGDCLPGRVYRKTGLVGFQDMCVPCGDPPPPPEHCASK 121
QY 153 VNLVVIKSTVSPRDTALAAVTCALATVLLALLILCVYCKRQFMEKPKPSWLSRSDIQ 212
DB 122 LSLVKYDAHTVPPREATLVALLVGLVLFALAFGLFLFYCKQIFNRH----- 169
QY 213 YNGSELSCFDRPOLHEYAHRACCCRRDSVQ-----TCGVRLLPSCCEACSPNATL 267
DB 170 -----CQC-RDSLQYAEKTVBEDSLFPVPPGQETSPPEPANE 206
QY 268 G 268
DB 207 G 207

RESULT 4
Q8BM50 ID Q8BM50 PRELIMINARY; PRT; 297 AA.
AC Q8BM50
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Similar to X-linked ectodysplasin-A receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK034909; BAC28879.1; -.
SQ SEQUENCE 297 AA; 33038 MW; D5F2CD188765AD65 CRC64;

Query Match 22.0%; Score 496; DB 11; Length 297;
Best Local Similarity 40.2%; Pred. No. 6.9e-38;
Matches 97; Conservative 30; Mismatches 74; Indels 40; Gaps 3;

QY 33 DCQQQBFDRSRGNCVPCNCGPMELSKCEGFGYGEDAQCVTCRLHRFKEDWGFQKCKPC 92
DB 2 DCQENEYRDQWGRCVTCQQCGPQOELSKDCGYGEGDAHCIVCPPRKYKSTWGHRCQTC 61
QY 93 LDCAVNVRQKANCSDATSDAICGDCLPGRVYRKTGLVGFQDMCVPCGDPPPPPEHCASK 152
DB 62 ITCAVINRVQKANCNTNTSNAICGDCLPGRVYRKTGLVGFQDMCVPCGDPPPPPEHCASK 121
QY 153 VNLVVIKSTVSPRDTALAAVTCALATVLLALLILCVYCKRQFMEKPKPSWLSRSDIQ 212
DB 122 LSLVKYDAHTVPPREATLVALLVGLVLFALAFGLFLFYCKQIFNRH----- 169
QY 213 YNGSELSCFDRPOLHEYAHRACCCRRDSVQ-----TCGVRLLPSCCEACSPNATL 267
DB 170 -----CQC-RDSLQYAEKTVBEDSLFPVPPGQETSPPEPANE 206
QY 268 G 268
DB 207 G 207
```



Db 2 DCQNEYRDWGRVCVTCCQCGQBLSKDCCGCGEGGDAHCIVCPRRKXKWTGHHRCOTC 61

QY 93 LDCAVNRFQKANCATSDAICGDLPGFYRKTGLVGFQDMCEVCPCGDPDPPEYEPHCASK 152

Db 62 ITCAVINRAQKANTNTSNAICGDLPRFYRKTGRIGLQDQECIPCTKTQTPSEVQCTFQ 121

QY 153 VNLVKIASTASPRDTALAANVCISALATVLLALLILCVYCKRQPMKPPSWLSRSDIQ 212

Db 122 LSLVKVDAHTVPPQEAVALVSSLLVVFALFLGLFLYCKQIF 166

QY 213 YNGSELSCFDRPQLHEYAHRAACCCQRDSVQ-----TCGPVRLPSMCCERACSPNPATL 267

Db 170 -----CQC-RDLSQYAEAKTVEEDSLFVPPGQETSPFPANE 206

QY 268 G 268

Db 207 G 207

RESULT 5

ID Q81ZA6 PRELIMINARY; PRT; 318 AA.

AC Q81ZA6;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE X-linked ectodermal dysplasia receptor long isoform.

GN XEDAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2232314; PubMed=12270937;

RA Sinha S.K., Zachariah S., Quinones H.I., Shindo M., Chaudhary P.M.,

RT "Role of TRAF3 and -6 in the Activation of the NF-kappa B and JNK

RT Pathways by X-linked Ectodermal Dysplasia Receptor.";

RL J. Biol. Chem. 277:44953-44961(2002).

DR EMBL; AY152724; AAN73210.1; -.

KW Receptor.

SQ SEQUENCE 318 AA; 34992 MW; A4C8AED32F346A3E CRC64;

Query Match 21.6%; Score 488; DB 4; Length 318;

Best Local Similarity 30.8%; Pred. No. 4.2e-37;

Matches 121; Conservative 50; Mismatches 110; Indels 112; Gaps 12;

QY 33 DCROQEFDRSGNCVPCNQCQPGMELSKGCGFYGEDAQCVTCRLHRFKEDWGFKCKPC 92

Db 2 DCQNEYRDWGRVCVTCCQCGQBLSKDCCGCGEGGDAHCIVCPRRKXKWTGHHRCOTC 61

QY 93 LDCAVNRFQKANCATSDAICGDLPGFYRKTGLVGFQDMCEVCPCGDPDPPEYEPHCASK 152

Db 62 ITCAVINRAQKANTNTSNAICGDLPRFYRKTGRIGLQDQECIPCTKTQTPSEVQCTFQ 121

QY 153 VNLVKIASTASPRDTALAANVCISALATVLLALLILCVYCKRQPMKPPSWLSRSDIQ 212

Db 122 LSLVKVDAHTVPPQEAVALVSSLLVVFALFLGLFLYCKQIF 166

QY 213 YNGSELSCFDRPQLHEYAHRAACCCQRDSVQTCGPVRLPSMCCERACSPNPATLGGCVH 272

Db 166 -----FNR-----HCQREKL-----IIFS-----DPVPASL----- 186

QY 273 SAASLQARNAGPAGMVTTPGSLTQSCIGSFSDANPLMQNPMGDNISFCDSPELTGE 332

Db 187 -----NLIPFAGGLQLQFEADTAKEESLFVPPPSKET-----SAESQVSE 227

QY 333 DI-----HSLNPELSSTSLDSSQDLVGGAVPVQSHSNFTAA----- 373

Db 228 NIFQTPNPLFLEDDCSSTS-----GFPTQ-----ESFTVASCTSESHSHWHVSPIC 275

QY 374 ---DLRYNNTLVESASTQDALTWRSQLDQESG 403

Db 276 TELDQKFSS-----SASYTGAETLGGNTVESTG 304

RESULT 6

Q8BJ56 PRELIMINARY; PRT; 185 AA.

ID Q8BJ56

AC Q8BJ56;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Similar to X-linked ectodysplasin-A receptor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; TISSUE=Aorta and vein;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK080072; BAC37822.1; -.

SQ SEQUENCE 185 AA; 20832 MW; 7335CCAC83C829C4 CRC64;

Query Match 21.5%; Score 486; DB 11; Length 185;

Best Local Similarity 49.7%; Pred. No. 3.3e-37;

Matches 82; Conservative 28; Mismatches 55; Indels 0; Gaps 0;

QY 33 DCROQEFDRSGNCVPCNQCQPGMELSKGCGFYGEDAQCVTCRLHRFKEDWGFKCKPC 92

Db 2 DCQNEYRDWGRVCVTCCQCGQBLSKDCCGCGEGGDAHCIVCPRRKXKWTGHHRCOTC 61

QY 93 LDCAVNRFQKANCATSDAICGDLPGFYRKTGLVGFQDMCEVCPCGDPDPPEYEPHCASK 152

Db 62 ITCAVINRAQKANTNTSNAICGDLPRFYRKTGRIGLQDQECIPCTKTQTPSEVQCTFQ 121

QY 153 VNLVKIASTASPRDTALAANVCISALATVLLALLILCVYCKRQIF 197

Db 122 LSLVKVDAHTVPPQEAVALVSSLLVVFALFLGLFLYCKQIF 166

RESULT 7

Q9PVD4 PRELIMINARY; PRT; 387 AA.

ID Q9PVD4

AC Q9PVD4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE P75-like transmembrane protein fullback.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;

RT "Identification and Characterization of fullback, a Novel Posteriorly-

RT Expressed Xenopus Gene.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF131890; AAD54072.1; -.

DR HSP; P07174; INGR.

DR InterPro; IPR00488; Death.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00017; DEATH DOMAIN; 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.



Db 911 IAAISMASKITDMLQGG-----VEISKLTITKEVHQARLECDCEBSALERKKR--LAEAF 964

Qy 361 PVQSHSENFTAAATDLSRYNNLTVESASTQDALTMRSQLDQSGAIHPATQTSIQ 415

Db 965 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLVEAVNKVEVE 1017

RESULT 10

Q96EL5 PRELIMINARY; PRT; 1120 AA.

AC Q96EL5; (Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strauberg R.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; BC012151; AAH12151.1; -.

DR InterPro; IPR001374; R3H.

DR InterPro; IPR006895; zf-Sec23\_Sec24.

DR InterPro; IPR000967; Znf\_NFX1.

DR InterPro; IPR001965; Znf\_PHD.

DR InterPro; IPR001841; Znf\_ring.

DR Pfam; PF01424; R3H; 1.

DR Pfam; PF00097; zf-C3HC4; 1.

DR Pfam; PF01422; zf-NFX1; 8.

DR Pfam; PF04810; zf-Sec23\_Sec24; 1.

DR SMART; SM00393; R3H; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00438; Znf\_NFX; 9.

DR PROSITE; PS00016; ZF\_PHD 2; 1.

DR PROSITE; PS00089; ZF\_RING 2; 1.

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 1120 AA; 124394 MW; F2203B1DB6437E6 CRC64;

Query Match 6.3%; Score 142; DB 4; Length 1120;

Best Local Similarity 18.8%; Pred. No. 0.00035;

Matches 110; Conservative 58; Mismatches 182; Indels 236; Gaps 27;

Qy 24 SKVTCESGDCRQEFRRDRSGVPCNQCQPGMELSKECG-----FGYGEDAQ----- 72

Db 456 SCNLLCHPG-----PCPPCPAFMTKTCCEGRTRHTVRCQAVSVHCSNPC 500

Qy 73 ---VTCRLHRFKEDWGFQCKPCCLDCAVVRPQKANCATS-DALCGDCLPGFYRKTLLV 128

Db 501 ENILNCGHQHAEILCHGQCQPCQ--IILN--QVCYCGSTRDLVLCGTDV-----GKSD 550

Qy 129 GFQDMEC-----VPCGD-----PPH-----PYEPHC--ASKVNLVKIATASS 164

Db 551 FGFDPSCLIKIGKDLKCGNHTCSQVCHPQPCQCPQLPQLVRCPCGQTPLSLELGS 610

Qy 165 PRDTALAAV-----IC-SALATVLLALLILC-----VIYCKRQFMKK- 201

Db 611 SRKTCMDVPSCGKVGKPLPGSLDFHTCEKLCHGDCGCPCSRTSVISCRCSFRTKEL 670

Qy 202 PSWLSRSDI-----QYNGSELSCFDRPQ-----LH---EYA 230

Db 671 PCTSLKSEDAFMCDKRCNKRKLCGRHKCNICCVDEKHKPLICGRKRLCGLHRCBEP 730

Qy 231 HRACQ-CRRDSVQT-----CGVRLPSMCC-----EE 258

Db 731 HRGNCQTCWQASFDLTCGASVIPPVCGTRPPECTQTCTCARVHECDHPVYHSCSE 790

Qy 259 ACS-----PNPATLGGVHSAASL----- 277

Db 791 KCPCTFTLQKCMGKHEFRSNIPCHLVDISCGLPSCSATLPCGMHMKQRLCHKGECLVDE 850

Qy 278 -----OAR-----NAGPAGEVMVPTFFGSLTQSI 300

Db 851 PKQCTPTPRADCGHPCMARHTSSPCVPTACKAKVBLQCECGRRKEKVICSEASITQR 910

Qy 301 CGEFSDAWLPQMPMGDNISFCDSYPPELTGDIHSLNPELESSTSLDSSQDLVGAV 360

Db 911 IAAISMASKITDMLQGG-----VEISKLTITKEVHQARLECDCEBSALERKKR--LAEAF 964

Qy 361 PVQSHSENFTAAATDLSRYNNLTVESASTQDALTMRSQLDQSGAI 406

Db 965 HISEDSDPFNIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 1008

RESULT 11

Q8BTVO PRELIMINARY; PRT; 436 AA.

AC Q8BTVO;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 19-like homolog.

DE Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NOD; TISSUE=Thymus;

RC MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium.

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL; AK088621; BAC40459.1; -.

SQ SEQUENCE 436 AA; 46518 MW; E61304480DBA0815 CRC64;

Query Match 6.2%; Score 141; DB 11; Length 436;

Best Local Similarity 22.0%; Pred. No. 0.00013;

Matches 71; Conservative 33; Mismatches 103; Indels 116; Gaps 15;

Qy 52 CGPMELSKECGFGYGEDAQCVTCRLHREFKEDWGFQCKPCCLDCAVVRPQKANCATS 111

Db 39 CPPKEDPDPGQ-----TLCTCPPTGTFASWNSYFCQPHYRCSLQKRLBAQAGTATHD 94

Qy 112 AICGDCPLPGFYRKTLLVGFQDMECVPCGDPDP-----P 144

Db 95 TMCQDCQHWGFPQ---GVPHVPCQPCSKAPPSTGGCGDESGRRGRRGVEVAAGTSSNGEP 151

Qy 145 YEPHCASKVNLVKIATASSPRDTALA-AVICSALATVLLALL--ILCVI-----YCKR 195

Db 152 RQPCNGTR-----AGPEETAQYAVIAIVPVFCLMGLLILVCLNLLKRYGYHCTA 202

Qy 196 QFMKKPS-----WSLSRSDI-----QYNGSE---LSCFDRPOLH 227

Db 203 Q-KEVGPSPGGGGINPAYRTEDANEDTIGLVRLITEKKENAAALEELLKEYHSKQLV 261

Qy 228 EYAHRAQCQRDRSVQTCGPV-RLLPSCMCCEACSPNPATILGCGVHSAASLQARNAGPAG 286

Db 262 QTSR-----FVPRLLPA-----SPSIPHCPIHHHLHTVQG----- 293

Qy 287 BMVPTFFGSLTQSIQCBFSDAWP 309

Db 294 -----LASLSGCCSCRSQKWP 310

RESULT 12

Q9GQ45 PRELIMINARY; PRT; 548 AA.

ID Q9GQ45

AC Q9GQ45;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DN Variant-specific surface protein M21-1 (Fragment).
GN M21-1.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ad-1;
RA Mansouri M., Ey P.L.;
RT "A segment of a vsp72-like gene homolog from a type A-I (group 1)
RT Giardia intestinalis isolate."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAG37862.1; -.
DR HSRF; P00136; 2CY3.
DR InterPro; IPR006058; 2Fe2S ferredoxin.
DR InterPro; IPR000345; CytC heme bind.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IEGF_repeat.
DR InterPro; IPR002350; kazal.
DR SMART; SM00181; EGF; 2.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00282; KAZAL; 1.
FT NON_TER 1 548
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FB4FDA0A2CF0E CRC64;

Query Match 6.2%; Score 140.5; DB 5; Length 548;
Best Local Similarity 24.3%; Pred. No. 0.0002;
Matches 69; Conservative 22; Mismatches 124; Indels 69; Gaps 16;

Qy 21 GYLSCK-----VTESGDCROEFRDRSGNVCNQCQPGMELSKGCGFYGEDAQCVTC 75
Db 182 GCIDCTGANQCTCEDGKYL-----KNQCVDAGQCDQGTADPTTG-----QCKPC 228

Qy 76 RLHRFKEDWGQCKPCLDCAVNRFPQKANCATSDAI-----C---GDCLPGFY 122
Db 229 -----GITDCATCEYNATISQPOCKTSSNNKVKTAADGTTTCVDGCGCTNG-- 277

Qy 123 RKTCLV-GFQDMECVPCDPPPYE---PHCASKVLVKIATASTASSPRDTALAAVIGSAL 178
Db 278 -NTHFVEGTNQLCVPCGDTTNGVLGNTCSSKTTCTK---CLDGYDSGSGTGTCTAC 333

Qy 179 ATVLLALLLCVYICKQFMKPSWSLSQDIQYNGSELSCFDRPQLHAYHRAACQCR 238
Db 334 PGANCA--TLCCRY-KRQCTTKCPGFFLKDSS---SGECISCDK---NNGHGCSACS 384

Qy 239 RDSVQTCGPVR-----LLPSMCCEBACSNPATLGGVHSA 275
Db 385 SNGAFKCTDCKPNYKKEGTSNDYTCVKTEDETA---CGGTSGA 425

RESULT 13
Q8JFV6 ID Q8JFV6 PRELIMINARY; PRT; 317 AA.
AC Q8JFV6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SI:d2107D16.1 (Novel protein similar to vertebrate nerve growth factor
DE receptor (NGFR). (Fragment).
GN SI:d2107D16.1.
OC Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
```

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RA Ramsay H.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591671; CAD43421.1; -.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
FT NON_TER 1 317
FT NON_TER 317
SQ SEQUENCE 317 AA; 34446 MW; D9B7EF1C70DAF92B CRC64;

Query Match 6.2%; Score 139; DB 13; Length 317;
Best Local Similarity 22.7%; Pred. No. 0.00014;
Matches 58; Conservative 25; Mismatches 113; Indels 60; Gaps 11;

Qy 21 GYLSCKVTC-ESGD---CRQOEFRD-RSGNVCNQCQPGMELSKGCGFYGEDAQCVT 74
Db 76 GLMRMOTPTCTDSNDAECVCNNGYFMNVLSRCEPCTVCPGLQGVDNRCELNH--DTVCEE 133

Qy 75 CRLHRFKEDWG-FQCKPCLDCAVNRFPQKANCATSDAICGCLD-PGFYRKTLYGVQD 132
Db 134 CRDETYSQDQNTMDPCMPCTICEEDTEILLRNCTPTEDALCHDPLSPYPTSTGDSGSD 193

Qy 133 MECVPCGDP-----PPPEPHCASK---VNLVKIATASSPRDTALAAVICSLATV 181
Db 194 TDLRLWSPSPGDDATTTPKSPSPHFGRGLNENLPI-----YCSILAAV 238

Qy 182 LLALLILCVI-----YCKR-----QFMKKPSWSLSQDIQYNGSE 217
Db 239 VUGLLAYIIFKRWNSCKNQKQAANRAATANTQTPSPGKGLHSDSGISVDSQSLQEQAAQ 298

Qy 218 LSCFDRPQLHAYHRA 233
Db 299 TOTQAQAQHTQLHAA 314

RESULT 14
O72735 ID O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AS3R protein.
GN AS3R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox, and vaccinia viruses."
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75273.1; -.
DR HSP; O92956; LTMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A0A0AE3 CRC64;

Query Match 6.1%; Score 138.5; DB 12; Length 186;
Best Local Similarity 28.0%; Pred. No. 7.8e-05;
Matches 46; Conservative 19; Mismatches 68; Indels 31; Gaps 11;
```

RESULT 15

Query Match	6.1%;	Score 136.5;	DB 12;	Length 350;
Best Local Similarity	26.9%;	Pred. No. 0.00027;		
Matches 43;	Conservative	19;	Mismatches 61;	Indels 37;
				Gaps 8;

Search completed: January 29, 2004, 21:40:00  
Job time : 42 secs

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